

GenCore version 5.1.6
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OM protein - nucleic search, (using frame_plus_p2n model
Run on: September 7, 2005, 16:41:11; Search time 403 Seconds
(without alignments)
3938.433 Million cell updates/sec

Title: US-10-026-021-2
Perfect score: 5078
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents.NA:
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5075	99.9	3937	4	US-09-620-312D-280
2	3927.5	77.3	3447	1	Sequence 280, App
3	3927.5	77.3	3447	1	Sequence 3, Appli
4	1967	38.7	1600	2	Sequence 3, Appli
5	1967	38.7	1600	2	Sequence 5, Appli
6	1883.5	37.1	1453	1	Sequence 5, Appli
7	1883.5	37.1	1453	1	Sequence 1, Appli
8	590.5	11.6	2169	4	Sequence 1, Appli
9	560.5	11.0	2770	3	Sequence 1147, Ap
10	560.5	11.0	2770	3	Sequence 8, Appli
11	560.5	11.0	2789	3	Sequence 8, Appli
12	560.5	11.0	2789	3	Sequence 3, Appli

13	538.5	10.6	2783	3	US-09-136-282-1	Sequence 1, Appli
14	538.5	10.6	2783	3	US-09-505-744-1	Sequence 1, Appli
15	533	10.5	2124	3	US-09-198-122-1	Sequence 1, Appli
16	526.5	10.4	4557	3	US-09-614-221A-446	Sequence 446, App
17	510.5	10.1	2033	3	US-09-660-925B-10	Sequence 10, Appl
18	508.5	10.0	2198	2	US-08-755-728-2	Sequence 2, Appli
19	508.5	10.0	2198	2	US-08-974-655-2	Sequence 2, Appli
20	508.5	10.0	2198	3	US-09-283-011-2	Sequence 2, Appli
21	508.5	10.0	2198	4	US-09-012-135A-2	Sequence 2, Appli
22	508.5	10.0	2237	4	US-09-949-016-4590	Sequence 4590, Ap
23	508.5	10.0	2237	4	US-09-949-016-4591	Sequence 4591, Ap
24	508.5	10.0	2253	3	US-09-660-925B-3	Sequence 3, Appli
25	500	9.8	1539	4	US-09-633-328B-1	Sequence 1, Appli
26	492.5	9.7	2224	4	US-09-949-016-2384	Sequence 2384, Ap
27	492.5	9.7	2224	4	US-09-949-016-2385	Sequence 2385, Ap
28	489.5	9.6	1815	4	US-09-485-534-3	Sequence 3, Appli
29	487	9.6	2175	4	US-09-984-890-1	Sequence 1, Appli
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31	485.5	9.6	1224	4	US-09-949-016-3955	Sequence 3955, Ap
32	485.5	9.6	1244	2	US-08-753-728-1	Sequence 1, Appli
33	485.5	9.6	1244	2	US-08-974-655-1	Sequence 1, Appli
34	485.5	9.6	1244	3	US-09-283-011-1	Sequence 1, Appli
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37	479.5	9.4	2950	4	US-09-949-016-1546	Sequence 1546, Ap
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39	477.5	9.4	1791	4	US-09-270-767-1985	Sequence 1985, Ap
40	477.5	9.4	1791	4	US-09-270-767-17267	Sequence 17267, A
41	477	9.4	993	4	US-09-248-796A-4394	Sequence 4394, Ap
42	473	9.3	1929	3	US-09-359-161-4	Sequence 4, Appli
43	468	9.2	3246	4	US-09-614-221A-228	Sequence 228, App
44	465.5	9.2	2912	4	US-09-949-016-2363	Sequence 2363, Ap
45	465	9.2	2899	4	US-09-774-528-112	Sequence 112, App

ALIGNMENTS

RESULT 1
US-09-620-312D-280
; Sequence 280, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Fang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Reivan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_fl_genes Version 1.0
; SEQ ID NO 280
; LENGTH: 3937
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (334)..(3246)
US-09-620-312D-280

Alignment Scores:
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Score: 5075.00 Matches: 969
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.90% Mismatches: 0
Query Match: 99.94% Indels: 0
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QY 61 ValLysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu 80
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QY 121 IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer 140
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Qy 961 MetPheSerAsnProThrProAsnPheHis 970

Db 3214 ATGTTTTCTAATCCGACTCTTAATTTTCAT 3243

RESULT 2

US-08-252-995D-3

; Sequence 3, Application US/08252995D

; Patent No. 5650501

; GENERAL INFORMATION:

; APPLICANT: Dennis, James W

; APPLICANT: Heffernan, Mike

; APPLICANT: Fode, Carol

; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BRESKIN & PARR

; STREET: 40 King Street West

; CITY: Toronto

; STATE: Ontario

; COUNTRY: Canada

; ZIP: M5H 3Y2

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/252,995D

; FILING DATE: 02-JUN-1994

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Kurdydk, Linda M

; REGISTRATION NUMBER: 34,971

; REFERENCE/DOCKET NUMBER: 3153-96

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (416) 364-7311

; TELEFAX: (416) 361-1398

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3447 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Mus musculus

; DEVELOPMENTAL STAGE: Lymphoid cDNA Library

; IMMEDIATE SOURCE:

; LIBRARY: Murine Lymphoid

; CLONE: WGA-resistant chop clones

; FEATURE:

; NAME/KEY: 5'UTR

; LOCATION: 1..205

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 206..2980

; FEATURE:

; NAME/KEY: 3'UTR

; LOCATION: 2981..3447

; US-08-252-995D-3

Alignment Scores:

Pred. No.: 0 Length: 3447

Score: 3927.50 Matches: 763

Percent Similarity: 86.41% Conservative: 76

Best Local Similarity: 78.58% Mismatches: 83

Query Match: 77.34% Indels: 49

DB: 1 Gaps: 9

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Db 566 ATCAGAGAAATGTAATCTTCATCTCATGGCATATTCACACCGGAGCTCACACTCTCT 625
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Db 686 TTGAATATGCCACATGAAAGACCATATACACTCTGTGGGACTCTCTAAATATATTTACCA 745
Qy 181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTyrSerLeuGlyCysMet 200
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Qy 359 ArgValIleGlnAspAlaGluArgProHisSerArgTyrLeuArgArgAlaTyrSer 378
Db 1280 AGAGTGATTAAGATGCAGAAAGAGCGCAATTCGATACCTCGCAGAGCTCTCTCC 1339
Qy 379 SerAspArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArg 398
Db 1340 TCTGATAGCCAGCCCTCTAAT---CAGTCTCGAGCAAAAAACATACACTCAGTAGAACGT 1396
Qy 399 CysHisSerAlaGluMetLeuSerValSerLysArgSerGlyGlyGlyGluAsnGluGlu 418
Db 1397 TGCTACTCAGTAGAATGCTTTCAAGCCCTAGAAATCA----- 1435
Qy 419 ArgTyrSerProThrAspAsnAlaAlaAsnIlePheAsnPhePheLysGluLysThrSer 438

Db 1435 ----- 1435
Qy 439 SerSerSerGlySerPheGluArgProAspAsnAsnGlnAlaLeuSerAsnHisLeuCys 458
Db 1436 -----CTGGATGAAATCAACACAGTTCCAATCATCATGTGT 1471
Qy 459 ProGlyLysThrProPheProPheAlaAspProThrProGlnThrGluThrValGlnGln 478
Db 1472 CTAGGAAAAATCTCTTTTCCATTTTCAGACAGACCTTCAGATGGAAATGGTACAGCAG 1531
Qy 479 TrpPheGlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrThrGluTyrAspSerIle 498
Db 1532 TGGTTTGGGAATCTGCAATGAATGATCTCATTTAGAGAAAATAATAGCACACACCGCTT 1591
Qy 499 SerProAsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLysAsnAla 518
Db 1592 AGCCCAACACAGATTTCCAGGACTATCCAGATTTTCAG---GACACGTTACGAAACGCT 1648
Qy 519 TrpThrAspThrLysValLysLysAsnSerAspAlaSerAspAsnAlaHisSerValLys 538
Db 1649 TGGACTGACAGAGAGCCAGCAAGAATGCTGATACTTCTGCCAATGTTTCATGCTGTAAAG 1708
Qy 539 GlnGlnAsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleIleGlnGln 558
Db 1709 CAGCTGAGTGCATGAATATACATGAGTGCAATCACCATAAGCCTGAGGTTCATGCCACAG 1768
Qy 559 GluCysValPheGlySerAspProLeuSerGluGlnSerLysThrArgGlyMetGluPro 578
Db 1769 GAGCG-----GGCCTACACTCTCACTCTGAACAAAGCAAGATAGAAGTATGGAGTCG 1822
Qy 579 ProTrpGlyTyrGlnAsnArgThrLeuArgSerIleThrSerProLeuValAlaHisArg 598
Db 1823 ACCTGGGTTTACCAGAAACCTTACCTTAAGAAGTATTACATCTCTCTGATTGCTCACAGA 1882
Qy 599 LeuLysProIleArgGlnLysThrLysLysAlaValValSerIleLeuAspSerGluGlu 618
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Qy 619 ValCysValGluLeuValLysGluTyrAlaSerGlnGluTyrValLysGluValLeuGln 638
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Qy 639 IleSerSerAspGlyAsnThrIleThrIleTyrProAsnGlyGlyArgGlyPhePro 658
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Qy 659 LeuAlaAspArgProProSerProThrAspAsnIleSerArgTyrSerPheAspAsnLeu 678
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Qy 699 LysSerProLysIleThrThrPheThrArgTyrAlaLysCysIleLeuMetGluAsnSer 718
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Qy 719 ProGlyAlaAspPheGluValTyrPheTyrAspGlyValLysIleHisLysThrGluAsp 738
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Qy 739 PheIleGlnValIleGluLysThrGlyLysSerTyrThrLeuLysSerGluSerGluVal 758
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Qy 759 AsnSerLysGluGluIleLysMetTyrMetAspHisAlaAsnGluGlyHisArgIle 778
Db 2363 ACCAGCTGAAAGAGGAGTAAAGATATATGAGCCATGCTAATAGGGGTCACCGTATT 2422
Qy 779 CysLeuAlaLeuGluSerIleIleSerGluGluGluArgLysThrArgSerAlaProPhe 798
Db 2423 TGCTTGCTACCTGGAATCTGTAAATCTCTGAGGAGGAAAGAGACGAGGGGTTCTTCAITTC 2482

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QY 799 PheProIleIleIleGlyArgLysProGlySerThrSerSerProLysAlaLeuSerPro 818
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QY 839 MetHisSerAlaAspSerProThrGlnAlaProIleLeuAsnProSerMetValThrAsn 858
Db 2600 GTGAATAGTGGCGCTTCCACACAGCTCCCGCAGGACTCAGTCTTCCACTGTGACAGTT 2659
QY 859 GluGlyLeuGlyLeuThrThrAlaSerGlyThrAspIleSerSerAsnSerLeuLys 878
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QY 879 AspCysLeuProLysSerAlaGlnLeuLeuLysSerValPheValLysAsnValGlyTrp 898
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QY 899 AlaThrGlnLeuThrSerGlyAlaValTrpValGlnPheAsnAspGlySerGlnLeuVal 918
Db 2765 GCTACACAGCTAACTAGCGGACTGTGTGGTTTCAAGTTTAAATGATGGTCCAGTTGGTT 2824
QY 919 ValGlnAlaGlyValSerSerIleSerTyrThrSerProAsnGlyGlnThrThrArgTyr 938
Db 2825 GTCCAGGAGGAGTAGTCTTCCATCAGTTACACATCACCAGATGGTCCAGAACTAGGTAT 2884
QY 939 GlyGluAsnGluLysLeuProAspTyrIleLysGlnLysLeuGlnCysLeuSerSerIle 958
Db 2895 GGAGAAATGAAATAATACCTGAAATACATCAACAGAAATACAGTGCTCTTCTTCCATC 2944
QY 959 LeuLeuMetPheSerAsnProThrProAsnPhe 969
Db 2945 CTTCTGATGTTTCTTAATCCAACTCTTAATTT 2977
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RESULT 3

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US-08-834-108-3
; Sequence 3, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; DEVELOPMENTAL STAGE: Lymphoid cDNA Library
; IMMEDIATE SOURCE:
; LIBRARY: Murine Lymphoid
; CLONE: WGA-resistant chop clones
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..205
; FEATURE: CDS
; NAME/KEY: LOCATION: 206..2980
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 2981..3447
US-08-834-108-3
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Alignment Scores:

Pred. No.:	0	Length:	3447
Score:	3927.50	Matches:	763
Percent Similarity:	86.41%	Conservative:	76
Best Local Similarity:	78.58%	Mismatches:	83
Query Match:	77.34%	Indels:	49
DB:	2	Gaps:	9

US-10-026-021-2 (1-970) x US-08-834-108-3 (1-3447)

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QY 21 GlySerPheAlaGlyValTyrArgNlaGluSerIleHisThrGlyLeuGluValLalle 40
Db 266 GGATCATTTGCTGGTGTCTACAGAGCTGAGTCCATACACACTGGTTTGGAAAGTTGCAATC 325
QY 41 LysMetIleAspLysLysAlaMetTyrLysAlaGlyMetValGlnArgValGlnAsnGlu 60
Db 326 ARAATGATAGATAGAAAGCCATGTACAAAGCTGGAAATGGTACAGAGAGTCCAAATGAG 385
QY 61 ValLysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu 80
Db 386 GTGAAATATACATTGCCAGTTGAAACACCCCTCTGTCTTGGAGCTCTATAATTTACTTTGAA 445
QY 81 AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyr 100
Db 446 GATAACAATATGTCTACCTGGTATTGGAAATGTGCCACAATGGAGAAATGAACAGATAT 505
QY 101 LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle 120
Db 506 CTGAAGAAACAGATGAAGCCCTTCTCAGAAAGGGAAGCTAGGACCTTCATGCACAGATT 565
QY 121 IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer 140
Db 566 ATCAGAGAAATGTTATATCTTCATCTCATGGCATATTTGCACCGGAGACTCACACTCTCT 625
QY 141 AsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGln 160
Db 626 AACATCTTACTTACGCGGAATATGAACATAAAAAATTTGCTGACTTTGGACTAGCAACGCG 685
QY 161 LeuLysMetProHisGluLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPro 180
Db 686 TTGAATATGCCACATGAAAGCACTATACACTCTGTGGGACTCTCTTAATATATTTTACCA 745
QY 181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTrpSerLeuGlyCysMet 200
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 Qy 241 LeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerValLeu 260
 Db 926 CTTATCCACCGATTACTTCGTAGAAACCTCGAGATCGTTAAGTCTGCTCTCTGTGTG 985
 Qy 261 AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu 280
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 Db 1163 AAAATTACTGTATTTCAAAAAATAAATTCAGTGACTTT---TCTTCAGGAGATCGA 1219
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 Db 1220 AGTAATTTTGTACTCAATGGGGAATCCAGAACAGAGAGCTAATAGTAGGGGACGGGG 1279
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 Qy 439 SerSerSerGlySerPheGluArgProAspAsnAsnGlnAlaLeuSerAsnHisLeuCys 458
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 Db 1532 TGGTTTGGAAATCTCGAATGAATGCTCATTTAGGAGAACTTAATGAGCACCACCGCTT 1591
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 Db 1592 AGCCCAACACAGAGATTTCCAGGACTATCCAGATTTCAG---GACACGTTACGAACGCT 1648
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 Db 1769 GAGCCG-----GGCCTACATCTCTGAACAAAGCAAGAAATAGAAGTATGGAGTCG 1822

Qy 579 ProTrpGlyTyrGlnAsnArgThrIleuArgSerIleThrSerProLeuValAlaHisArg 598
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 Qy 599 LeuLysProIleArgGlnLysThrLysLysAlaValValSerIleLeuAspSerGluGlu 618
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 Db 2483 TTCCCTATATCGTAGGAAGAAAAACCTGGTAAATAGTTTCCCTCAAAGCCTTATCAGCT 2542
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 Db 2543 CCTCCT---GTGGACCCCAAGCTGCTGTAAGGGAGAGAGCGGCTCAGCAAGCAGACTGAGC 2599
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QY 959 LeuLeuMetPheSerAsnProThrProAsnPhe 969
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RESULT 4

US-08-252-995D-5
; Sequence 5, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252.995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34, 971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1600 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; DEVELOPMENTAL STAGE: Lymphoid cDNA Library
; IMMEDIATE SOURCE:
; LIBRARY: Murine lymphoid
; CLONE: WGA-resistant chop clones
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..205
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 206..1597
US-08-252-995D-5
Alignment Scores:
Pred. No.: 8,72e-192 Length: 1600
Score: 1967.00 Matches: 385
Percent Similarity: 92.0% Conservative: 34
Best Local Similarity: 84.62% Mismatches: 30
Query Match: 38.74% Indels: 7
Dbs: 1 Gaps: 5
US-10-026-021-2 (1-970) x US-08-252-995D-5 (1-1600)
QY 1 MetaAlaThrCysIleGlyGluLysIleGluAspPheLysValGlyAsnLeuGlyLys 20

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QY 81 AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyr 100
Db 446 GATAACAATTTATGTCTACCTGGTATTGGAAATGTGCCCAATGGAGAAATGACACATAT 505
QY 101 LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle 120
Db 506 CTGAAGAACACAGATGAAGCCCTTTCTCAGAAAGGGAAGCTAGGCACCTTCATGCACCAGATT 565
QY 121 IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer 140
Db 566 ATCAGAGGAATGTTATATCTTCATTTCTCATGGCATATTGCACCGGAGCCTCACACTCTCT 625
QY 141 AsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGln 160
Db 626 AACATCTTACTTACGGGAATATGAACATAAAATTTGCTGACTTTGGACTAGCAACGAG 685
QY 161 LeuLysMetProHisGluLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPro 180
Db 686 TTGAATATGCCACATGAAAGCACATATACACTCTGTGGGACTCTCTAATATATATTTACCA 745
QY 181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTrpSerLeuGlyCysMet 200
Db 746 GAAATTCACACTCGAAGTGCACTGGACTTGAATCTGTATATTGGTTCATTGGGCTGTATG 805
QY 201 PheTyrThrLeuLeuIleGlyArgProPheAspThrAspThrValLysAsnThrLeu 220
Db 806 TCTTATAGTTTACTATTATGGGAAGACCCTTTTGACACTGACACAGTCAAGAAGACATG 865
QY 221 AsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAsp 240
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QY 241 LeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerSerValLeu 260
Db 926 CTTATCCACCAGTTACTTCGTAGAAACCTTCAGATCGGTTAAGTCTCTCTCTGTGTG 985
QY 261 AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu 280
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QY 321 LysMetThrValPheProLysAsnLysSerSerThrAspPheSerSerSerSerGlyAsp 340
Db 1163 AAAATTAAGTGTATTTCAAAAAATAAAATTTCAAGTGTGACTTT---TCTTCAGGAGATGGA 1219
QY 341 AsnSerPheTyrThrGlnTyrGlyAsn-----GlnGluThrSerAsnSerGlyArgGly 358
Db 1220 AGTAATTTTGTACTCAATGGGGAATCCAGAACAGAGAGCTAATAGTAGGGGACGGGG 1279
QY 359 ArgValIleGlnAspAlaGluArgProHisSerArgTyrLeuArgArgAlaTyrSer 378

Db 1280 AGAGTGATTGAAGATGCAGAGAGCGCGCATTCCTCGATACCTCGCGCAGAGCTCATTC 1339
 QY 379 SerAspArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArg 398
 Db 1340 TCTGATGAGCGCCGCTCTTAAT---CAGTCTCGAGCAAAACATACCTAGTAGAAGCT 1396
 QY 399 CysHisSerAlaGluMetLeuSerValSerLysArgSerGlyGlyGlyGluAsnGlu 418
 Db 1397 TGTCACTCAGTAGAAGTCTTTCAAGAGCTAGAGATCA---CTGGATGAAATCAACAC 1453
 QY 419 ArgTyrSerProThrAspAsnAlaAsnIlePheAsnPhePheLysGluLysThrSer 438
 Db 1454 AGGTATTCAACCCACCAAGCAATGCTCAATGT-TTTAACTTCATTAAACACCAACAGCC 1512
 QY 439 SerSerSerGlySerPheGluArgProAspAsnGlnAlaLeu 453
 Db 1513 AATAGTTAAGGATCTTTTGAAGACCGGTATATGACTGAGCAGTA 1557

RESULT 5

US-08-834-108-5
 ; Sequence 5, Application US/08834108
 ; Patent No. 5976893
 ; GENERAL INFORMATION:
 ; APPLICANT: Dennis, James W
 ; APPLICANT: Heffernan, Mike
 ; APPLICANT: Fode, Carol
 ; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BERESKIN & PARR
 ; STREET: 40 King Street West
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5H 3Y2
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/834,108
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kurydyk, Linda M
 ; REGISTRATION NUMBER: 34,971
 ; REFERENCE/DOCKET NUMBER: 3153-210
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 364-7311
 ; TELEFAX: (416) 361-1398
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; TYPE: nucleic acid
 ; LENGTH: 1600 base pairs
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: Mus musculus
 ; DEVELOPMENTAL STAGE: Lymphoid cDNA Library
 ; IMMEDIATE SOURCE:
 ; LIBRARY: Murine Lymphoid
 ; CLONE: WGA-resistant chop clones
 ; FEATURE:
 ; NAME/KEY: 5'UTR
 ; LOCATION: 1..205
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 206..1597
 ; US-08-834-108-5

Alignment Scores:

Pred. No.:	8,72e-192	Length:	1600
Score:	1967.00	Matches:	385
Percent Similarity:	92.09%	Conservative:	34
Best Local Similarity:	84.62%	Mismatches:	30
Query Match:	38.74%	Indels:	7
DB:	2	Gaps:	5

US-10-026-021-2 (1-970) x US-08-834-108-5 (1-1600)

QY	1	MetAlaThrCysIleGlyGluLysValGlyAsnLeuGlyLys	20
Db	206	ATGCGCGGTCATCGCGGAGGATCGAGACTTTAAGGTTGGAATCTACTCGGTAA	265
QY	21	GlySerPheAlaGlyValTyrArgAlaGluSerIleHisThrGlyLeuGluValAlaIle	40
Db	266	GGATCATTTGCTGTGTCTACAGAGCTGAGTCCATACACACTGGTTTGGAAAGTTGCAATC	325
QY	41	LysMetIleLeuPheLysAlaMetTyrIleValGlyMetValGlnArgValGlnAsnGlu	60
Db	326	AAAATGATAGATAAGAACCCATGTACAAAGCTGGAATGGTACAGAGAGTCCAAATGAG	385
QY	61	ValLysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu	80
Db	386	GTGAAATACATTCGCCAGTTGAAACACCCCTCTGCTTGGAGCTCTATAATTAATCTTGAA	445
QY	81	AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyr	100
Db	446	GATAACAATTTATGCTTACCTGTTTGAATGTGCCACATATGGAGAAATGAACAGATAT	505
QY	101	LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle	120
Db	506	CTGAAGAACAGATGAAGCCCTTCTCAGAAAGGGAAGCTAGGCACCTTCATGCACAGATT	565
QY	121	IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer	140
Db	566	ATCACAGGAATGTTATATCTTCATCTCATGGCATATTCACCGGGACCTTCACACTCTCT	625
QY	141	AsnLeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGln	160
Db	626	AACATCTTACTACGCGGAATATGAACATAAAATTCGTGACTTTGGACTAGCAACGAG	685
QY	161	LeuLysMetProHisGluLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPro	180
Db	686	TTGAATATGCCACATGAAAGCACTATACACTCTGTGGGACTCTCTAAATTAATTTACCA	745
QY	181	GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTyrSerLeuGlyCysMet	200
Db	746	GAAATTCGAACCTCGAAGTGACATGGACTTGAATCTGATATTTGGTCATTGGCGCTGATG	805
QY	201	PheTyrThrLeuLeuIleGlyArgProPheAspThrAspThrValLysAsnThrLeu	220
Db	806	TCATTATAGTTACTTATTGGAAGACCACCTTTTGACACTGACACAGTCAAGAACACATG	865
QY	221	AsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAsp	240
Db	866	AACAAAGTAGTCTGGCAGATTATGAATGCCACCTTTTGTTCAGAGAGCCCGCAGAC	925
QY	241	LeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerSerValLeu	260
Db	926	CTTATCCACCAAGTTACTTCGTAGAAACCCCTGCAGATCGGTTAAGTCTCTCTCTGTGTG	985
QY	261	AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu	280
Db	986	GACCATCTTTTCATGTCTACGAAATCCTTTCACCAAGAGATAAGAGCTAGGAGCTGTAG	1045
QY	281	AspSerIleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerSerThr	300
Db	1046	GACTCAATGATAGTGGCATGCTACACTTTCCACACAAATTAAGCCCTCTCTCTGTGTACC	1105
QY	301	SerIleSerGlySerLeuPheAspLysArgArgLeuLeuIleGlyGlnProLeuProAsn	320
Db	1106	AGTTTGAGTGGCAGCTACTTGTAC---AGAAGACTTTTGGTTGGTCAACCACTTCCAAAT	1162

QY 321 LysMetThrValPheProLysAsnLysSerSerThrAspPheSerSerSerGlyAspGly 340
Db 1163 AAAATTACTGATTTTCAAAAAATAAAATTCAGTGACTTT---TCITCAGGAGATGGA 1219
QY 341 AsnSerPheTyrThrGluTyrGlyAsn-----GlnGluThrSerAsnSerGlyArgGly 358
Db 1220 AGTAATTTTGTACTCAATGGGGAATCCAGAACGAAGAGCTTAATAGTAGGGGAGGGGG 1279
QY 359 ArgValIleGlnAspAlaGluArgProHisSerArgTyrLeuArgAlaTyrSer 378
Db 1280 AGAGTGATTGAAGATGCAGAGAGAGCGCATTCCTCGATACCTCGCGAGAGCTCATTC 1339
QY 379 SerAspArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArg 398
Db 1340 TCTGATAGAGCCAGCCCTCTAAT---CAGTCTCAGCAAAAACATACCTCAGTAGAAGCT 1396
QY 399 CysHisSerAlaGluMetLeuSerValSerLysArgSerGlyGlyGlyGluAsnGlu 418
Db 1397 TGTCTACTCAGTAGAATGCTTTCAAGCGCTAGAAGATCA---CTGGATGAAATCAACAC 1453
QY 419 ArgTyrSerProThrAspAsnAlaAsnIlePheAsnPhePheLysGluLysThrSer 438
Db 1454 AGGTATTCACCCACCAAGCAATGTCATGT-TTTAACTTCATTAAACACCAACAGCC 1512
QY 439 SerSerSerGlySerPheGluArgProAspAsnAsnGlnAlaLeu 453
Db 1513 AATAGTAAAGATCTTTTGAAGACCGTATATAGTACTGAGCAGTA 1557

RESULT 6

US-08-252-995D-1
; Sequence 1, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3V2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1453 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; DEVELOPMENTAL STAGE: Lymphoid cDNA Library
; IMMEDIATE SOURCE:
; LIBRARY: Murine Lymphoid

; CLONE: WGA-Resistant Chop Clones
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 206..1453
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..205
US-08-252-995D-1
Alignment Scores:
Pred. No.: 2,85e-183 Length: 1453
Score: 1883.50 Matches: 362
Percent Similarity: 94.19% Conservative: 27
Best Local Similarity: 87.65% Mismatches: 19
Query Match: 37.09% Indels: 5
DB: 1 Gaps: 4
US-10-026-021-2 (1-970) x US-08-252-995D-1 (1-1453)
QY 1 MetAlaThrCysIleGlyGluLysValGlyAsnLeuGlyLys 20
Db 206 ATGGCGCGTGCATCGGGGAGGATCGAGACTTTAAAGTTGGAAATCTACTCGGTAAA 265
QY 21 GlySerPheAlaGlyValTyrArgAlaGluSerIleHisThrGlyLeuGluValAlaIle 40
Db 266 GGATCAATTTGCTGCTGTCTACAGAGCTGAGTCCATACACACTGGCTTTGGAAGTTGCAATC 325
QY 41 LysMetIleAspLysLysAlaMetTyrLysAlaGlyMetValGlnArgValGlnAsnGlu 60
Db 326 AAAATGATAGATAAGAAGCCATGTACAAAGCTGGAATGGTACAGAGAGTCCAAAATGAG 385
QY 61 ValLysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu 80
Db 386 GTGAAATATACATTCGCCAGTTGAAACACCCCTCTGCTTGGAGCTCTATAATTACTTTGAA 445
QY 81 AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyr 100
Db 446 GATAACCAATTTATGCTACCTGGTATTGGAATGTGCCAATGTGCCAATGTGGAATGAACAGATAT 505
QY 101 LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle 120
Db 506 CTGAAGAACAGAAATGAAGCCCTTTCTCAGAAAGGAAAGCTAGGCACCTTCATGCACCAAGATT 565
QY 121 IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer 140
Db 566 ATCACAGGAATGTTATATCTTCATTTCTCATGGCATATTGACCGGGACCTCACACTCTCT 625
QY 141 AsnLeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGln 160
Db 626 AACATCTTACTTACGCGGAATATGAACATAAAATTTGCTGACTTTGGACTAGCAACGCGAG 685
QY 161 LeuLysMetProHisGluLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPro 180
Db 686 TTGAATATGCCACATGAAAGACACTATACACTCTGTGGGACTCCTAAATATATTATTTCACCA 745
QY 181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTyrSerLeuGlyCysMet 200
Db 746 GAAATTCGAATCTGAAAGTGCACATGGACTTGAATCTGATATTGCTCATTTGGGCTGTATG 805
QY 201 PheTyrThrLeuLeuIleGlyArgProPheAspThrAspThrValLysAsnThrLeu 220
Db 806 TCTTATACGTTTACTTATTGGAAGACCACTTTTCACACTGCACACTGCACAGACACACTTG 865
QY 221 AsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAsp 240
Db 866 AACAAAGTAGTCTCTGGCAGATTTATGAAATGTCACCTTTTGTCCAGGAGGCGCCAGGAC 925
QY 241 LeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerValLeu 260
Db 926 CTTATCCACCAAGTTACTTCGTAGAAACCTCCACATCGTGAAGTCTGCTCTCTCTGTGTG 985
QY 261 AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu 280

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Db 986 GACCATCTCTTTCATGTCACGAAATCCTTCCACCAAGAGTAAAGACGTAGGAGCTGTAGAG 1045
Qy 281 AspSerIleAspSerGlyHisIaThrIleSerThrAlaIleThrAlaSerSerThr 300
Db 1046 GACTCAATGGATAGTGGGCATCTACACTTTCACAACAATTTACAGCCTCTTCTGGTACC 1105
Qy 301 SerIleSerGlySerIlePheAspLysArgArgLeuLeuIleGlyGlnProLeuProAsn 320
Db 1106 AGTTTGGTGGCAGCTACTTGAC---AGAGACCTTTTGGTGGTCAACCACTTCCAAT 1162
Qy 321 LysMetThrValPheProLysSerLysSerSerThrAspPheSerSerSerGlyAspGly 340
Db 1163 AAAATTACTGTATTTCAAAAAATAAAATTCAGTGACTTT---TCTTCAGGAGATGGA 1219
Qy 341 AsnSerPheTyrThrGlnTrpGlyAsn-----GlnGluThrSerAsnSerGlyArgGly 358
Db 1220 AGTAATTTTGTACTCAATGGGGAATCCAGAACAGAGCTAATAGTAGGGGACGGGG 1279
Qy 359 ArgValIleGlnAspAlaGluArgProHisSerArgTyrLeuArgArgAlaTyrSer 378
Db 1280 AGAGTGATGATGAGATGCAGAGAGGCGCATTTCTCGATACCTCGCAGAGCTCATTC 1339
Qy 379 SerAspArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArg 398
Db 1340 TCTGATAGAGCAGCCCTCTAAT---CAGTCTCGAGCAAAAACATACCTCAGTAGAACGT 1396
Qy 399 CysHisSerAlaGluMetLeuSerValSerLysArgSer 411
Db 1397 TGTCACTCAGTAGAATAATGCTTTCAAAGCCTAGAGATCA 1435
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RESULT 7

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US-08-834-108-1
; Sequence 1, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurodyck, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1453 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; DEVELOPMENTAL STAGE: Lymphoid cDNA Library
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; IMMEDIATE SOURCE:
; LIBRARY: Murine Lymphoid
; CLONE: WGA-Resistant Chop Clones
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 206..1453
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..205
US-08-834-108-1
Alignment Scores:
Pred. No.: 2,85e-183 Length: 1453
Score: 1883.50 Matches: 362
Percent Similarity: 94.19% Conservatives: 27
Best Local Similarity: 87.65% Mismatches: 19
Query Match: 37.09% Indels: 5
DB: 2 Gaps: 4
US-10-026-021-2 (1-970) x US-08-834-108-1 (1-1453)
Qy 1 MetAlaThrCysIleGlyGluLysIleGluAspPheLysValGlyAsnLeuLeuGlyLys 20
Db 206 ATGGCGCGTGCATCGGGAGAGGATCGAGCACTTTAAGGTTGGAATCTACTCGGTAA 265
Qy 21 GlySerPheAlaGlyValTyrArgAlaGluSerIleHisThrGlyLeuGluValAlaIle 40
Db 266 GGATCATTTGCTGGTGTCTACAGAGCTGAGTCCATACACACTGGTTTGGAAAGTTGCAATC 325
Qy 41 LysMetIleAspLysLysAlaMetTyrLysAlaGlyMetValGlnArgValGlnAsnGlu 60
Db 326 AAAATGATAGATAAGAAAGCCATGTACAACTGGATGGATGTCACAGAGTCCAAAATGAG 385
Qy 61 ValLysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu 80
Db 386 GTGAAATATACATTGCCAGTTGAAACACCCCTCTCTCTGGAGCTCTATAATTTACTTTGAA 445
Qy 81 AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyr 100
Db 446 GATAACAATTTATGTCTACCTGGTATTGGAATGTGCCCAATGGAGAAATGAACAGATAT 505
Qy 101 LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle 120
Db 506 CTGAAGAACAGATGAAGACCTTTCTCAAGAGGAGGAGCTAGGCACTTCATGCCACAGATT 565
Qy 121 IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrIleuSer 140
Db 566 ATCAGAGGAATGTTATATCTTCAATTCATGGCATATTGCCACCGGACCTCACACTCTCT 625
Qy 141 AsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGln 160
Db 626 AACATCTTACTTCGCGGAATATGAACATAAAAATTTGCTGACTTTGGACTAGCAACGAG 685
Qy 161 LeuLysMetProHisGluLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPro 180
Db 686 TTGAATATGCCACATGAAGACACTATACACTCTGTGGGACTCTCTAATATATTTTACCA 745
Qy 181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTrpSerLeuGlyCysMet 200
Db 746 GAAATTCGAACCTCGAAGTGACATGGACTTGAATCTGTATATTGGTTCATTGGGCTGTATG 805
Qy 201 PheTyrThrLeuLeuIleGlyArgProPheAspThrAspThrValLysAsnThrLeu 220
Db 806 TCTTATACGTTACTTATTTGGAAGACCACTTTTGACACTGACACAGTCAAGAACACATTTG 865
Qy 221 AsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAsp 240
Db 866 AACAAAGTAGTCTGGCAGATTATGAATGCGCCCTTTTGTTCACGAGAGCCCGAGAC 925
Qy 241 LeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerValLeu 260
Db 926 CTTATCCACCACTTACTTTCGTAGAAACCCCTGCAGATCGGTTAAGTCTCTCTCTCTGTG 985
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QY 261 AspHisProPheMetSerArgLysSerThrLysSerLysSerLysLeuGlyThrValGlu 280
Db 986 GACCATCTCTTTTATGTCAGCAATCTTCCACCAAGAGTAAAGACCTAGGACTGTAGAG 1045
QY 281 AspSerIleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerThr 300
Db 1046 GACTCAATGATAGTGGGATGCTACCTTCCACCAACATTTACAGCCTCTTCTGGTACC 1105
QY 301 SerIleSerGlySerLeuPheAspLysArgArgLeuLeuIleGlyGlnProLeuProAsn 320
Db 1106 AGTTTGGAGTGGCAGCTACTTGCAC--AGAAGACTTTTGGTTGGTGAACCACTTCCAAAT 1162
QY 321 LysMetThrValPheProLysLysSerSerThrAspPheSerSerSerGlyAspGly 340
Db 1163 AAAATTACTGTATTTCAAAAAATAAAATTCAGTGACTTTT--TCTTCAGGAGATGGA 1219
QY 341 AsnSerPheTyrThrGlnTyrGlyAsn-----GlnGluThrSerAsnSerGlyArgGly 358
Db 1220 AGTATTTTGTACTCAATGGGGAATCCAGAACAGAGAGCTAAATAGTAGGGGAGCGGGG 1279
QY 359 ArgValIleGlnAspAlaGluArgProHisSerArgTyrLeuArgArgAlaTyrSer 378
Db 1280 AGAGTGATTAAGATGCGAAGAGAGGCGGCATTCTCGATACCTGGCAGAGCTCATTC 1339
QY 379 SerAspArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArg 398
Db 1340 TCTGATAGACGAGCCCTCTTAAT---CAGTCTCGAGCAAAACATACCTCAGTAGACGT 1396
QY 399 CysHisSerAlaGluMetLeuSerValSerLysArgSer 411
Db 1397 TGCTACTCAGTAGAAATGCTTTCAAGCCTAGAAGATCA 1435
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RESULT 8

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US-09-016-434-1147
; Sequence 1147, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016.434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2169 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1488262
US-09-016-434-1147
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Alignment Scores:

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Pred. No.: 5,77e-50 Length: 2169
Score: 590.50 Matches: 115
Percent Similarity: 57.33% Conservative: 61
Best Local Similarity: 37.46% Mismatches: 106
Query Match: 11.63% Indels: 25
DB: 4 Gaps: 4
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US-10-026-021-2 (1-970) x US-09-016-434-1147 (1-2169)

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QY 15 GlyAsnLeuLeuGlyLysGlySerPheAlaGlyValTyrArgAlaGluSerIleHisThr 34
Db 112 GCGCGCTTGTGGGCAAGGGGGCTTCGCCCGCTGCTACGAGGCCACTGCACAGAGACT 171
QY 35 GlyLeuGluValAlaIleLysMetIleAspLysLysAlaMetTyrLysAlaGlyMetVal 54
Db 172 GCGAGCGCTACGCTGTCAAAGTCAATCCGAGAGCCGCGTCCGCAAGCCGATCAGCGC 231
QY 55 GlnArgValGlnAsnGluValLysIleHisCysGlnLeuLysHisProSerIleLeuGlu 74
Db 232 GAGAAGATCTCTAAATGAGATTGAGCTGCACCGAGACCTGCAGACCGCCACATCGTCGT 291
QY 75 LeuTyrAsnTyrPheGluAspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsn 94
Db 292 TTTTCGCACCACTTTTGAGGAGCTGCACCACTACATTTCTTTGGAGCTCTGCACCGCA 351
QY 95 GlyGluMetAsnArgTyrLeuLysAsnArgValLysProPheSerGluAsnGluAlaArg 114
Db 352 AAGTCCCTGGCCCATCTCGAAGCCCGG---CACACCCTGTGTGAGCCAGAGTGGCGC 408
QY 115 HisPheMetHisGlnIleIleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHis 134
Db 409 TACTACCTGGCGGAGATCTCTTTCTGGCTCAAGTACTTGCACGCGCGGATCTTGCAC 468
QY 135 ArgAspLeuThrLeuSerAsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAsp 154
Db 469 CGGGACCTCAAGTTGGGAAATTTTTCATCACTCAGAAACATGGAACATGAAGTGGGGAT 528
QY 155 PheGlyLeuAlaThrGlnLysMetProHisGluLysHisTyrThrLeuCysGlyThr 174
Db 529 TTTGGCTGGCAGCCCGCTTGGAGCCTCCGAGAGCAGAGAGAACACATCTGTGGCACC 588
QY 175 ProAsnTyrIleSerProGluIleAlaThrArgSerAlaHisGlyLeuGluSerAspVal 194
Db 589 CCCAACTATGTGGCTCCAGAGTGTCTGTGAGACAGGCGCCACGCGCTGAAGCGGATGTA 648
QY 195 TrpSerLeuGlyCysMetPheTyrThrLeuLeuIleGlyArgProProPheAspThrAsp 214
Db 649 TGGTCACTGGGCTGTGTCACTACACGCTGTCTCGGGGAGCCCTCCCTTTTGAAGCGGT 708
QY 215 ThrValLysAsnThrLeuAsnLysValValLeuAlaAspTyrGluMetProSerPheLeu 234
Db 709 GACCTGAAGGAGAGCTACCGCTGTCAAGCAGGTTCATACGCTGCTCCCTGCCGCTC 768
QY 235 SerIleGluAlaLysAspLeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeu 254
Db 769 TCACCTGCTGCCCGGAGCTCTCGCGCCCATCTCTCGGGCTCACCCCGGAGACGCGCCC 828
QY 255 SerLeuSerSerValLeuAspHisProPheMetSerArgAsnSerSerThrLysSerLys 274
Db 829 TCTATTGACAGATCTCGCGCATGACTCTTTTACCAAG----- 867
QY 275 AspLeuGlyThrValGluAspSerIleAspSerGlyHisAlaThrIleSerThrAlaIle 294
Db 868 -----GGCTACACCCCGCATCGACTC-----CCTATCAGCAGCTGCGGTG 906
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QY 395 ThrMetGluArgCysHisSerAlaGluMetLeuSerValSerIysArgSerGlyGly 414
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Db 1346 ACAGATGAGGAGCTCCAGCCACCT-----ACCACACAGATGTCAGGCTCGAACACCC 1399
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QY 415 GluAsnGluArgTyrSerProThrAspAsnAlaAsnIlePheAsnPhePheLys 434
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Db 1400 GCAGTAGAACAACAGCAGAGATGGGATGCTATTCCGATGATAGTCAGAGGACTCTT 1459
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QY 435 GluLysThrSerSerSerGlySerPheGluArgProAspAsnAsnGln----- 451
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Db 1460 GCAGCTGTAGCAGCAGCAGTGAATGCCTTGA-----GACATACCATGGGAAGTGT 1513
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QY 452 -----AlaLeuSerAsnHisLeuCysProGlyLys 461
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Db 1514 GCAGACACAGTGCAGAGGTTCTTCGGGATGCTCGAAAAAC----- 1555
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QY 462 ThrProPheProPheAlaAsp-----ProThrProGlnThrCluThrValGlnGlnTTP 479
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Db 1556 -----ATCGCGAAGCTGATTGCATTCCCAAGACGCTGAGCACATCATTTTCAGTGG 1609
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QY 480 -----PheGlyAsnLeuGlnIleAsnAla 487
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Db 1610 CTCACAAATGGTGTACTTACTTAACAATATGGCTTTGGG---TACCAGCTCTCAGAC 1666
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QY 488 HisLeuArgLysThrThrGluTyrAspSerIleSerProAsnArgAspPheGlnGlyHis 507
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Db 1667 CACAC-CGTGG-----TGCTCTTTCAACAATGGTCTCACAT 1704
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QY 508 -----ProAspLeuGlnLysAspThrSer-----LysAsnAlaTTP 519
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Db 1705 GAGCTCTCTCCAGACAAAAAAGCTCACTATTACGAGAGCTTGG 1752
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RESULT 10

US-09-272-796-8
; Sequence 8, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166
TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2770 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVEB01
; CLONE: 39043
US-09-272-796-8

Alignment Scores:
Pred. No.: 1.09e-46 Length: 2770
Score: 560.50 Matches: 163
Percent Similarity: 44.03% Conservative: 73
Best Local Similarity: 30.41% Mismatches: 200
Query Match: 11.04% Indels: 101
DB: 3 Gaps: 18

US-10-026-021-2 (1-970) x US-09-272-796-8 (1-2770)

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QY 35 GlyLeuGluValAlaIleLysMetIleAspLysAlaMetTyrLysAlaGlyMetVal 54
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Db 413 AACAAAGTCTACGCGCAAAATATTCTCTCACAGAGTAGCTAAACCTCATCAAGG 472
|||
QY 55 GlnArgValGlnAsnGluValLysIleHisCysGlnLeuLysHisProSerIleLeuGlu 74
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Db 473 GAAAGATTGACAAAGAAATAGAGCTTCACAGAAATTTTCATCATAAAGCATGTAGTGCA 532
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QY 75 LeuTyrAsnTyrPheGluAspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsn 94
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QY 95 GlyGluMetAsnArgTyrLeuLysAsnArgValLysProPheSerGluAsnGluAlaArg 114
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Db 593 AGGTCAATGGCTCATATTTTGAACAGAGA---AAGTGTTCACAGAGCCAGAGTTGCA 649
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QY 115 HisPheMetHisGlnIleIleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHis 134
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Db 650 TACTACCTCAGCAGATTTGTCTGACTGAAATACCTTCATGAACAAGAAATCTTGAC 709
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QY 135 ArgAspLeuThrLeuSerAsnLeuLeuThrArgAsnMetAsnIleLysIleAlaAsp 154
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QY 195 TrpSerLeuGlyCysMetPheTyrThrLeuLeuIleGlyArgProProPheAspThrAsp 214
|||
Db 890 TGGGCGCTGGGCTGTGTAATGTATACAATGTATTACTAGGAGGCGCCCATTTGAAACTACA 949
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QY 215 ThrValLysAsnThrLeuAsnLysValValLeuAlaAspTyrGluMetProSerPheLeu 234
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Db 950 AATCTCAAGAAACATTTATAGGTGTCATAGGGAAGCAAGGTATACATGCGCTCATTTG 1009
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QY 235 SerIleGluAlaLysAspLeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeu 254
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Db 1010 CTGGCTCTGCGCAAGCACTTAATTCTAGTAGTTGTTCAAAAACCCAGAGAGATGCTCCC 1069
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QY 255 SerLeuSerSerValLeuAspHisProPheMetSerArgAsnSerSerThrLysSerLys 274
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Db 1070 AGTTGGATGACATCATCGACATCTTTTTCGAG----- 1108
Qy 275 AspLeuGlyThrValGluAspSerIleAspSerGlyHisAlaThrIleSerThrAlaIle 294
Db 1109 -----GGCTTCACTCCGACAGACTG----- 1129
Qy 295 ThrAlaSerSerThrSerIleSerGlySerLeuPheAspLysArgLeuLeuIle 314
Db 1130 -----TCCTCAGCTGTGTCTATCAGTTCAGAT-----TTCACATTA 1168
Qy 315 GlyGlnProLeuProAsnLysMetThrValPheProLysAsnLysSerSerThrAspPhe 334
Db 1169 TCAAGCCCACTAAGAAAT-----TTCCTTAAGAAAGCAGCTGCTCTCTTTT 1216
Qy 335 SerSerSerGlyAspGlyAsnSerPheThrGlnTrpGlyAsnGlnGluThrSerAsn 354
Db 1217 GGTGCCAAAAGACAAAGCAAGATATAT-----GACACATAAT 1258
Qy 355 SerGlyArgGlyArgValIleGlnAspAlaGluArgProHisSerArgTrpLeuArg 374
Db 1259 -----AGATGCTTAAGAGATGAAGACATCTCAAGCTTAGGCAT----- 1300
Qy 375 ArgAlaTyrSerSerAspArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyr 394
Db 1301 -----GATTTGAAAAGACTTCAATACTCACAACCCAGCAACACACAGG 1345
Qy 395 ThrMetGluArgCysHisSerAlaGluMetLeuSerValSerLysArgSerGlyGly 414
Db 1346 ACAGATGAGGAGTCCAGCCACCT-----ACCACCACAGTTGCCAGGTCTGGAACACCC 1399
Qy 415 GluAsnGluGluArgTyrSerProThrAspAsnAlaAsnIlePheAsnPhePheLys 434
Db 1400 GCAGTAGAAAACAAAGCAGAGATGGGATGCTATTTCGATGATAGTCAGAGGACTCTT 1459
Qy 435 GluLysThrSerSerSerGlySerPheGluArgProAspAsnAsnGln----- 451
Db 1460 GCAGCTGTAGCAGCAGCAGTGAATGCCCTTGAA-----GACAGTACCATGGGAAGTGT 1513
Qy 452 -----AlaLeuSerAsnHisLeuCysProGlyLys 461
Db 1514 GCAGACACAGTGGCAAGGTTCTTCGGGATGCTCTGAAAC----- 1555
Qy 462 ThrProPheProPheAlaAsp-----ProThrProGlnThrGluThrValGlnGlnTrp 479
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Qy 480 -----PheGlyAsnLeuGlnIleAsnAla 487
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Qy 488 HisLeuArgLysThrThrGluTyrAspSerIleSerProAsnArgAspPheGlnGlyHis 507
Db 1667 CACAC-CGTGCG-----TGTCTCTTTCAACAATGGTGTCTCAT 1704
Qy 508 -----ProAspLeuGlnLysAspThrSer-----LysAsnAlaTrp 519
Db 1705 GAGCTCTCTCCAGACAAAAAACAGCTCACTATTACGAGAGCTTGG 1752

RESULT 11
US-09-136-282-3
; Sequence 3, Application US/09136282
; Patent No. 6063609
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, KAREN
; APPLICANT: JACKSON, JEFFREY
; APPLICANT: HANSBURY, MICHAEL
; APPLICANT: NERURKAR, SANDHYA
; APPLICANT: ROSHAK, AMY
; APPLICANT: BOUZYK, MARK
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
```

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; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,282
; FILING DATE: 20-AUG-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,112
; FILING DATE: 20-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-136-282-3

Alignment Scores:
Pred. No.: 1,1e-46 Length: 2789
Score: 560.50 Matches: 163
Percent Similarity: 44.03% Conservative: 73
Best Local Similarity: 30.41% Mismatches: 200
Query Match: 11.04% Indels: 101
DB: 3 Gaps: 18

US-10-026-021-2 (1-970) x US-09-136-282-3 (1-2789)
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Qy 35 GlyLeuGluValAlaIleLysMetIleAspLysLysAlaMetTyrLysAlaGlyMetVal 54
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Qy 55 GlnArgValGlnAsnGluValLysIleHisCysGlnLeuLysHisProSerIleLeuGlu 74
Db 490 GAAAAGATTGACAAAGAAATAGAGCTTCACAGAATTCCTCATCATACAGCATGTAGTCAG 549
Qy 75 LeuTyrAsnTyrPheGluAspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsn 94
Db 550 TTTTACCACCTACTTCGAGGACAAAAGAAAATTTACATTTCTCTTGAATACTGTCAGTAGA 609
Qy 95 GlyGluMetAsnArgTyrLeuLysAsnArgValLysProPheSerGluAsnGluAlaArg 114
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Qy 115 HisPheMetHisGlnIleIleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHis 134
Db 667 TACTACCTCAGCAGATTGTCTGGAATTAACCTTCATGAAACAGAAATCTTGAC 726
Qy 135 ArgAspLeuThrLeuSerAsnLeuLeuThrArgAsnMetAsnIleLysIleAlaAsp 154
Db 727 AGAGATCTCAAACTAGGGAACCTTTTTTATTAATGAAGCCAGTGAACATAAAGTTGGGAC 786
Qy 155 PheGlyLeuAlaThrGlnLeuLysMetProHisGluLysHisTyrThrThrLeuCysGlyThr 174
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Db 490 GAAAGATTGACAAAGAAATAGAGCTTCACAGAAATTCATCATTAAGCATGTAGTCGAG 549
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Db 550 TTTTACCCTACTTCGAGGACAAAGAAACATTTACATCTCTTGGATACTGCAAGTAGA 609
Qy 95 GlyGluMetAsnArgTyrLeuLysAsnArgValLysProPheSerGluAsnGluAlaArg 114
Db 610 AG-GCAATGGCTCATATTTTGAAGCAAGA---AAGGTGTTGACAGAGCCAGAAGTTGGA 665
Qy 115 HisPheMetHisGlnIleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHis 134
Db 666 TACTACCTCAGGCAAGATTGTCTGAGCTGAATACCTTCATGAAACAAGAAATCTTGGCAC 725
Qy 135 ArgAspLeuThrLeuSerAsnLeuLeuThrArgAsnMetAsnIleLysIleAlaAsp 154
Db 726 AGAGATCTCAAACTAGGACCTTTTATTATTAAGGACCATGAAGTAAAGTTGGGAC 785
Qy 155 PheGlyLeuAlaThrGlnLeuLysMetProHisGluLysHisTyrThrLeuCysGlyThr 174
Db 786 TTGCGTCTGGCAGCCAGGCTAGAACCTTGGAAACACAGAGGAGAACGATATGTGTACC 845
Qy 175 ProAsnTyrIleSerProGluIleAlaThrArgSerAlaHisGlyLeuGluSerAspVal 194
Db 846 CCAAAATTAATCTCTCCCTGAAGTCTCAACAAACAGGACATGGCTGTGAATCAGACATT 905
Qy 195 TrpSerLeuGlyCysMetPheTyrThrLeuLeuIleGlyArgProPheAspThrAsp 214
Db 906 TGGGCGCTGGGCTGTGTAATGATACATGTTACTAGGAGGCCCCCAITTTGAAACTACA 965
Qy 215 ThrValLysAsnThrLeuAsnLysValValLeuAlaAspTyrGluMetProSerPheLeu 234
Db 966 AATCTCAAGAAACTTATAGGTGCATAGGGAAGCAAGTATACAAATGCCGTCTCATTTG 1025
Qy 235 SerIleGluAlaLysAspLeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeu 254
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Qy 255 SerLeuSerSerValLeuAspHisProPheMetSerArgAsnSerSerThrLysSerLys 274
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Qy 275 AspLeuGlyThrValGluAspSerIleAspSerGlyHisAlaThrIleSerThrAlaIle 294
Db 1125 -----GGCTTCACTCCGACAGACTG----- 1145
Qy 295 ThrAlaSerSerSerThrSerIleSerGlySerLeuPheAspLysArgArgLeuLeuIle 314
Db 1146 -----TCTTCTAGCTGTTGTGCATACATGTTCCAGAT-----TTCACACTA 1184
Qy 315 GlyGlnProLeuProAsnLysMetThrValPheProLysAsnLysSerSerThrAspPhe 334
Db 1185 TCAAGCCCAAGTAAAGAT-----TTCCTTAAGAAAGCAGCTGCTGCTCTTTT 1232
Qy 335 SerSerSerGlyAspGlyAsnSerPheTyrThrGlnTyrGlyAsnGlnGluThrSerAsn 354
Db 1233 GGTGCAAAAGACAAAGCAAGATATATT-----GACACATATAT 1274
Qy 355 SerGlyArgGlyArgValIleGlnAspAlaGluArgProHisSerArgTyrLeuArg 374
Db 1275 -----AGAGTGTCTAAAGAAAGTGAAGACATCTACAAGCTTAGGCAT----- 1316
Qy 375 ArgAlaTyrSerSerAspArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyr 394
Db 1317 -----GATTGAAAGACTTCAATACTCAGCAACCCAGCAACACACAGG 1361
Qy 395 ThrMetGluArgCysHisSerAlaGluMetLeuSerValSerLysArgSerGlyGlyGly 414
Db 1362 ACAGATGAGGAGCTCCAGCCACT-----ACCACACAGTTCGACAGCTCTGGAACACCC 1415
Qy 415 GluAsnGluArgTyrSerProThrAspAsnAsnAlaAsnIlePheAsnPhePheLys 434

Db 1416 GCAGTAGAAAAACAACAGACGACGATTGGGGATGCTATTTCGGATGATAGTCAGAGGGACTCTT 1475
Qy 435 GluLysThrSerSerSerGlySerPheGluArgProAspAsnAsnGln----- 451
Db 1476 GGCAGCTGTACGACGACGAGTGAATGCTTGA-----GACAGTACCATTGGAAAGTGT 1529
Qy 452 -----AlaLeuSerAsnHisLeuCysProGlyLys 461
Db 1530 GCAGACACAGTGGCAAGGTTCTTCGGGGATGTCTGGAAGAAC----- 1571
Qy 462 ThrProPheProPheAlaAsp-----ProThrProGlnThrGluThrValGlnGlnTyr 479
Db 1572 -----ATGCCGGAAGCTGATTTGCATTTCCAAAGAGCAGCTGAGCACATCATTTCACTGG 1625
Qy 480 -----PheGlyAsnLeuGlnIleAsnAla 487
Db 1626 GTCACCAAAATGGTGTATTACTCTAACAAATATGCTTTTGGG---TACCAGCTCTCAGAC 1682
Qy 488 HisLeuArgLysThrThrGluTyrAspSerIleSerProAsnArgAspPheGlnGlyHis 507
Db 1683 CACAC-CGTGCG-----TGTCCTTTTCAACAATGGTGTCTCACAT 1720
Qy 508 -----ProAspLeuGlnLysAspThrSer-----LysAsnAlaTyr 519
Db 1721 GAGCCTCTCTCCAGACAAACAAACAGTTTCACTATTACGACGAGCTTGG 1768

RESULT 14

US-09-505-744-1
; Sequence 1, Application US/09505744
; Patent No. 6245544
; GENERAL INFORMATION:
; APPLICANT: Karen M. Anderson
; APPLICANT: Mark M. Bouzyk
; APPLICANT: Michael J. Hansbury
; APPLICANT: Jeffrey R. Jackson
; APPLICANT: Sandhya S. Nerurkar
; APPLICANT: Amy K. Roshak
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
; FILE REFERENCE: GH-70231-D1
; CURRENT APPLICATION NUMBER: US/09/505,744
; CURRENT FILING DATE: 2000-02-16
; EARLIER APPLICATION NUMBER: 09/136,282
; EARLIER FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 60/056,112
; EARLIER FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2783
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (2720) (2721)
US-09-505-744-1

Alignment Scores:

Pred. No.: 2,01e-44 Length: 2783
Score: 538.50 Matches: 163
Percent Similarity: 44.03% Conservative: 73
Best Local Similarity: 30.41% Mismatches: 200
Query Match: 10.60% Indels: 102
DB: 3 Gaps: 18

US-10-026-021-2 (1-970) x US-09-505-744-1 (1-2783)

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292  Qy  ThrAlaIleThrAlaSerSerThrSerIleSerGlySerLeuPheAsp----- 308
1013 Db  ACCTGCTGACCAATCCACCAAGTTTTCATTGCTCCAGCAGCTGGACCCCGACCAAC 1072
309  Qy  ---LysArgArgLeuLeuIleGlyGlnProLeuProAsnLysMetThrValPheProLys 327
1073 Db  CGGAAGCCCTCACAGTCTCTCATAAAGCTTGGAGNACCCCTCGCTGAGCGTCCCGG 1132
328  Qy  AsnLysSerSerThrAspPheSerSerSerGlyAspGly-----AsnSer 342
1133 Db  GAAAAAGAGAACCAAGTGGTTCGAGAGACAGGTGAGTGGTTCGACTGCCACCTCAGTGAC 1192
343  Qy  PheTyrThrGlnTrpGlyAsnGlnGluThrSerAsn---SerGlyArgGlyArgValIle 361
1193 Db  ATGCTGAGCAGCTGCACAGTGTCAATGCTCCAAAGCCCTCGAGGCTGGGTGGTCAAG 1252
362  Qy  GlnAspAlaGluGluArgPro 368
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Job time : 465 secs

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GenCore version 5.1.6
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(without alignments)
4445.378 Million cell updates/sec
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 7338684 seqs, 3274456166 residues
Total number of hits satisfying chosen parameters: 14677368
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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5078	100.0	2913	14	US-10-026-021-1
2	5075	99.9	3937	15	US-10-037-270-280
3	5075	99.9	3937	17	US-10-117-722-280
4	5071	99.9	3721	14	US-10-116-802-108
5	5067	99.8	3092	20	US-10-737-450-89
6	5057	99.6	3331	21	US-10-887-553A-750
7	4861	95.7	2836	18	US-10-425-114-2625A
8	4777.5	94.1	3924	17	US-10-062-674-1868
9	743	14.6	484	10	US-09-918-995-21560
10	594	11.7	328	9	US-09-878-178-96
11	594	11.7	328	13	US-10-046-335-96
12	594	11.7	328	14	US-10-146-502-96
13	590.5	11.6	2169	14	US-10-108-580-1
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15	590.5	11.6	2169	17	US-10-305-720-1147
16	590.5	11.6	2169	19	US-10-304-116-4
17	590.5	11.6	2169	19	US-10-620-052A-27
18	590.5	11.6	2169	21	US-10-781-581-215
19	590.5	11.6	2378	19	US-10-755-889-3
20	590.5	11.6	2535	19	US-10-618-941-34
21	589.5	11.6	2410	19	US-10-304-116-12
22	567.5	11.2	2781	17	US-10-191-803-222
23	567.5	11.2	2781	18	US-10-152-319A-1953
24	567.5	11.2	2781	21	US-10-764-420-538
25	564.5	11.1	2772	21	US-10-764-420-944
26	560.5	11.0	2770	10	US-09-769-970-8
27	560.5	11.0	2783	15	US-10-024-298A-102
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29	560.5	11.0	2783	16	US-10-617-217A-102
30	560.5	11.0	2783	20	US-10-024-298A-102
31	560.5	11.0	2972	16	US-10-269-909-72
32	560.5	11.0	2972	17	US-10-172-118-1302
33	560.5	11.0	2972	17	US-10-159-563-102
34	560.5	11.0	2972	18	US-10-342-887-1302
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37	560.5	11.0	2972	21	US-10-782-413-94
38	560.5	11.0	2976	17	US-10-264-049-949
39	560.5	11.0	3024	14	US-10-198-846-11031
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41	545.5	10.7	2955	19	US-10-437-963-34025
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43	536	10.6	2137	19	US-10-283-975A-283
44	536	10.6	2137	21	US-10-487-422-88
45	536	10.6	2137	21	US-10-487-422-102

ALIGNMENTS

RESULT 1
US-10-026-021-1
; Sequence 1, Application US/10026021
; Publication No. US20030027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Demo, Susan
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; PRIORITY FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01

; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 2913
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (2)..(2913)
 ; OTHER INFORMATION: human SAK serine/threonine kinase
 US-10-026-021-1

Alignment Scores:

Pred. No.: 0 Length: 2913
 Score: 5078.00 Matches: 970
 Percent Similarity: 100.00% Conservativity: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-10-026-021-2 (1-970) x US-10-026-021-1 (1-2913)

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 QY 101 LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMethHisGlnIle 120
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 QY 121 IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer 140
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 DB 481 CTGAAATGCCATGCAAGAACACTATACATTATGTGGAACTCTCAACTACATTTTACCACA 540
 QY 181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTrpSerLeuGlyCysMet 200
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 QY 281 AspSerIleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerSerThr 300
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 DB 1261 TCACCCACAGACAACATGCCAACATTTTAACTTCTTTAAAGAAAAACATCCAGTAGT 1320
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QY 861 LeuGlyLeuThrThrThrAlaSerGlyThrAspIleSerSerAsnSerLeuLysAspCys 880
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QY 881 LeuProLysSerAlaGlnLeuLysSerValPheValLysAsnValGlyTrpAlaThr 900
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QY 901 GlnLeuThrSerGlyAlaValTrpValGlnPheAsnAspGlySerGlnLeuValValGln 920
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RESULT 2

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US-10-037-270-280
; Sequence 280, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghaast, John
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt FL_genes Version 1.0
; SEQ ID NO 280
; LENGTH: 3937
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (334)..(3246)
US-10-037-270-280

Alignment Scores:
Pred. No.: 0 Length: 3937
Score: 5075.00 Matches: 969
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.90% Mismatches: 0
Query Match: 99.94% Indels: 0
DB: 15 Gaps: 0

US-10-026-021-2 (1-970) x US-10-037-270-280 (1-3937)

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QY 21 GlySerPheAlaGlyValTyrArgAlaGluSerIleHisThrGlyLeuGluValAlaIle 40
Db 394 GGATCATTTGCTGGTGCTCTACAGACTGAGTCCATTCACACTGGTTTGGAGTTGCAATC 453
QY 41 LysMetIleAspLysLysAlaMetTyrLysAlaGlyMetValGlnArgValGlnAsnGlu 60
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QY 61 ValIlyIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu 80
Db 514 GTGAAAAATACATTCGAATTCGAATTCCTTCTATCTTGGAGCTTTATAACTATTTTGA 573
QY 81 AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyr 100
Db 574 GATAGCAATTATGTATCTGGTATTAGAAATGTGCCAATATGGAGAAATGAACAGGTAT 633
QY 101 LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle 120
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Db 634 CTAAGAATAGAGTGAACCCCTTCTCAGAAAAATGAAGCTCGACACTTCATGACCAGATC 693
QY 121 lIeThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer 140
Db 694 ATCACAGGATGTTGATCTTCATTTCTCATGTTATACACCGGACCTCACACTTCT 753
QY 141 AsnLeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGln 160
Db 754 AACCTCTACTGACTCGTGAATATGAACATCAAGATTCGTGATTTTGGGCTGGCAACTCAA 813
QY 161 LeuLysMetProHisGlyLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPro 180
Db 814 CTGAAAATGCCACATGAAAAGCACATATACATTTATGTGGNACTCTTAACATCATTTTCAACA 873
QY 181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTTPSerLeuGlyCysMet 200
Db 874 GAAATGGCCACTCGAAGTCACATGGCCTTGAATCTGATGTTTGGTCCCTGGGCTGTATG 933
QY 201 PheTyrThrLeuLeuIleGlyArgProProPheAspThrAspThrValLysAsnThrLeu 220
Db 934 TTTTATACATTTACTTATCGGGAGACACCCCTTCGACACTGCACAGTCAAGAACACATTA 993
QY 221 AsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAsp 240
Db 994 AATAAGTAGTATTGGCAGATTATGNAATGCCAATCTTTTGTCTCAATAGAGGCCAAGGAC 1053
QY 241 LeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerSerValLeu 260
Db 1054 CTTATTCCACAGTTACTTCGTAGAAATCCAGCAGATCGTTTAACTCTGCTTTCAGTATTG 1113
QY 261 AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu 280
Db 1114 GACCATCTCTTTATGTCGCGAATCTTCAACAAAAAGTAAAGATTTTAGGAACTGTGGAA 1173
QY 281 AspSerIleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerSerThr 300
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QY 301 SerIleSerGlySerLeuPheAspLysArgArgLeuLeuIleGlyGlnProLeuProAsn 320
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QY 321 LysMetThrValPheProLysAsnLysSerSerThrAspPheSerSerSerGlyAspGly 340
Db 1294 AAAATGACTGTATTTCCAAAGAAATAAAGTTCAACTGATTTTCTCTTCAGAGATGGA 1353
QY 341 AsnSerPheTyrThrGlnTTPGlyAsnGlnGluThrSerAsnSerGlyValArgVal 360
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QY 381 ArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArgCysHis 400
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QY 401 SerAlaGluMetLeuSerValSerLysArgSerGlyGlyGluAsnGluGluArgTyr 420
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Db 1594 TCACCACACAGACAAACAAATGCCAACAATTTTAACTCTTAAAGAAAAGACATCCAGTAGT 1653
QY 441 SerGlySerPheGluArgProAspAsnAsnGlnAlaLeuSerAsnHisLeuCysProGly 460
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QY 461 LysThrProPheProPheAlaAspProThrProGlnThrGluThrValGlnGlnTTPPhe 480
Db 1714 AAAACTCTTTTCCATTTTCAGACCCGACACCTCAGACTGAAACCGTACAAACAGTGGTTT 1773

QY 481 GlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrThrGluTyrAspSerIleSerPro 500
Db 1774 GGGAAATCTGCAAAATAAAATGCTCATTTAAGAAAAACTACTGAATATGACAGCATCAGCCCA 1833
QY 501 AsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLysAsnAlaTTPThr 520
Db 1834 AACCGGAGCTTCCAGGCGCATCCAGATTTCAGAAAGGACACATCAAAAAATGSCCTGGAAT 1893
QY 521 AspThrLysValLysLysAsnSerAspAlaSerAspAsnAlaHisSerValLysGlnGln 540
Db 1894 GATCAAAAAGTCAAAAAGAACTCTGATGCTTCTGATAATGCACATTCGTATAAACAGCAA 1953
QY 541 AsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleLeuGlnGlnCys 560
Db 1954 AATACCATGAAATATATGACTGCACTTCACAGTAAACCTGAGATAAATCCAAACAAGAAATGT 2013
QY 561 ValPheGlySerAspProLeuSerGluGlnSerLysThrArgGlyMetGluProProTTP 580
Db 2014 GTTTTGGCTCAGATCTCTTTCTGAAACAGAGCAAGACTAGGGGTATGGAGCCACCATGG 2073
QY 581 GlyTyrGlnAsnArgThrLeuArgSerIleThrSerProLeuValAlaHisArgLeuLys 600
Db 2074 GGTATCAGAAATCGTACATTAAGAGCATTACATCTCCGTGGTTGCTCAGAGTTAAAA 2133
QY 601 ProfileArgGlnLysThrLysLysAlaValValSerIleLeuAspSerGluGluValCys 620
Db 2134 CCAATCAGACAGAAAAACAAAAGGCTGTGTGAGCATACTTGATTCAGAGAGGTGTGT 2193
QY 621 ValGluLeuValLysGluTyrAlaSerGlnGluTyrValLysGluValLeuGlnIleSer 640
Db 2194 GTGAGCTTGTAAAGGAGTATGCATCTCAAGAAATATGTGAAAGAGTTCTTTCAGATATCT 2253
QY 641 SerAspGlyAsnThrIleThrIleTyrTyrProAsnGlyGlyArgGlyPheProLeuAla 660
Db 2254 AGTGATGGAATAACATCACTATTATATCAAAATGGTGTAGAGGTTTCTCTTGTCT 2313
QY 661 AspArgProProSerProThrAspAsnIleSerArgTyrSerPheAspAsnLeuProGlu 680
Db 2314 GATAGACACCTCACCTACTCTACAAACATCAGTAGGTACAGCTTTTGACAAATTTACCAGAA 2373
QY 681 LysTyrTTPArgLysTyrGlnTyrAlaSerArgPheValGlnLeuValArgSerLysSer 700
Db 2374 AAATACTGGCGAAATAATCAATATGCTTCCAGGTTTGTACAGCTTTGTAAGATCTAAATCT 2433
QY 701 ProLysIleThrTyrPheThrArgTyrAlaLysCysIleLeuMetGluAsnSerProGly 720
Db 2434 CCAAAATCACTTATTTACAAGATATGCTAAATGCAATTTTGTATGGAGAAATCTCTCGT 2493
QY 721 AlaAspPheGluValTTPPheTyrAspGlyValLysIleHisLysThrGluAspPheIle 740
Db 2494 GCTGATTTTGAGGTTTGGTTTTATGATGGGTAATAATATACAAAAACAGAAAGATTTTCAT 2553
QY 741 GlnValIleGluLysThrGlyLysSerTyrThrLeuLysSerGluSerGluValAsnSer 760
Db 2554 CAGTGATTTGAAAAGACAGGGAAGTCTTTACACTTTAAAGAGTGAAGTGAATTAATAGC 2613
QY 761 LeuLysGluGluIleLysMetTyrMetAspHisAlaAsnGluGlyHisArgIleCysLeu 780
Db 2614 TTGAAAGAGGAGATATAAATGCTATATGACCATGCTAATGAGGGTCATCGTATTTGTTA 2673
QY 781 AlaLeuGluSerIleLysSerGluGluArgLysThrArgSerAlaProPhePhePro 800
Db 2674 GCATCGGAATCCAAATTTTCAGAAAGAGAAAGAAAACTAGGAGTGTCTCCCTTTTCCCA 2733
QY 801 IleIleIleGlyArgLysProGlySerThrSerProLysAlaLeuSerProProPro 820
Db 2734 ATAATCATAGAAAGAAAAACCTGGTAGTACTAGTTCACCTTAAGGCTTATACCTCTCTCT 2793
QY 821 SerValAspSerAsnTyrProThrArgAspArgAlaSerPheAsnArgMetValMethis 840
Db 2794 TCTGTGGATTCAAATTTACCCCAACGAGATAGAGCATCTTTCAACAGAAATGGTCTGAT 2853

QY 841 SerAlaAseProThrGlnAlaProIleLeuAseProSerMetValThrAseGluGly 860
DB 2854 AGTGTGCTTCCTCCACACAGACCAATCCTTAATCCCTCTATGGTTACAAATGAAGA 2913
QY 861 LeuGlyLeuThrThrAlaSerGlyThrAspIleSerSerAseSerLeuLysAspCys 880
DB 2914 CTTGGCTTACAACTACAGCTTCTGGAACAGACATCTCTTAATAGTCTAAAGATGT 2973
QY 881 LeuProLysSerAlaGlnLeuLeuLysSerValPheValLeuAseValGlyTrpAlaThr 900
DB 2974 CTTCTTAATCAGCAACATTTTGAATCTGTTTTGTGAAAAATGTTGGTTGGGTACA 3033
QY 901 GlnLeuThrSerGlyAlaValTrpValGlnPheAseAspGlySerGlnLeuValGln 920
DB 3034 CAGTTAACTAGTGGAGCTGTGGGTTCAGTTTAATGATGGGTGCCAGTTGGTGGCAG 3093
QY 921 AlaGlyValSerSerIleSerIleThrSerProAseGlyGlnThrThrArgTrpGlyGlu 940
DB 3094 GCAGGAGTGTCTTCTATCATGTTATACCTCACCAATGGTCAAACTAGGTATGAGAA 3153
QY 941 AseGluLeuLeuProAspTrpIleLysGlnLysLeuGlnCysLeuSerSerIleLeuLeu 960
DB 3154 AATGAAAAATACCAGACTACATCAACACAGAAATACAGTGTCTGTCTTCCATCCTTTG 3213
QY 961 MetPheSerAseProThrProAsePheHis 970
DB 3214 ATGTTTTCTTAATCCGACTCCTTAATTTTCAT 3243

RESULT 3

US-10-117-722-280
; Sequence 280, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP28CIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 280
; LENGTH: 3937
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (334)..(3246)
US-10-117-722-280

Alignment Scores:

Pred. No.: 0 Length: 3937
Score: 5075.00 Matches: 969
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.90% Mismatches: 0
Query Match: 99.94% Indels: 0
DB: 17 Gaps: 0

US-10-026-021-2 (1-970) x US-10-117-722-280 (1-3937)

QY 1 MetAlaThrCysIleGlyLysIleGluAsePheLysValGlyAseLeuLeuGlyLys 20
DB 334 ATGGCGACCTGCATCGGGGAGAGATCGAGGATTTTAAAGTTTGAAGTCTGCTTGTGTTAA 393

QY 21 GlySerPheAlaGlyValTyArgAlaGluSerIleHisThrGlyLeuGluValAlaIle 40
DB 394 GGATCATTTGCTGGTGTCTACAGAGCTGAGTCCATTCACACTGGTTTGAAGTTGCAATC 453
QY 41 LysMetIleAsePheLysAlaMetTyLysAlaGlyMetValGlnArgValGlnAseGlu 60
DB 454 AAAATGATAGATAAGAAAGCCATGTACAAAGCAGGAATGGTACAGAGAGTCCAAATGAG 513
QY 61 ValLysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyAsnTrpPheGlu 80
DB 514 GTGAAATACATTTGCCAATTCGAACATCTTCTATCTTGGAGCTTTATAACTATTTTGA 573
QY 81 AseSerAseTrpValTyLeuValLeuGluMetCysHisAseGlyGluMetAseAsnArgTrp 100
DB 574 GATAGCAATTTATGTTATCTGTTATTAAGAAATGTCCATAATGGCAAGAAATGAACAGGTAT 633
QY 101 LeuLysAseAsnArgValLysProPheSerGluAseGlnAlaAArgHisPheMetHisGlnIle 120
DB 634 CTAAGAATAAGAGTGAACCCCTTCTCAGAAATGAAGCTCGACACTTCATGACCAGATC 693
QY 121 IleThrGlyMetLeuTyLeuHisSerHisGlyIleLeuHisArgAsePheLeuThrLeuSer 140
DB 694 ATCAGAGGATGTTGTTATCTTCTATCTGTTATCTGTTATCTGTTATCTGTTATCTGTT 753
QY 141 AseLeuLeuLeuThrArgAseMetAseIleLysIleAlaAsePheGlyLeuAlaThrGln 160
DB 754 AACCTCTACTGACTCGTAAATGAACATCAAGATTGCTGATTTTGGCTGGCAACTCAA 813
QY 161 LeuLysMetProHisGluLysHisTyThrLeuCysGlyThrProAseTrpIleSerPro 180
DB 814 CTGAAATGGCCACATGAAAGCATTATATGTTGAACTCTTAATCTTACACTTTCACCA 873
QY 181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAseValTrpSerLeuGlyCysMet 200
DB 874 GAATTTGCCACTCGAAGTGCATGGCTTGAATCTGATGTTGTTGCTTCTGCTGCTGATG 933
QY 201 PheTyThrLeuLeuIleGlyArgProPheAspThrAspThrValLysAseThrLeu 220
DB 934 TTTTATACATTTACTTATCGGAGACCCCTTCGACACTGACACAGTCAAGAACACATTA 993
QY 221 AseLysValValLeuAlaAseTyTrpClnMetProSerPheLeuSerIleGluAlaLysAsp 240
DB 994 AATAAGTAGTATTTGGCAGATTTATGAAATGCCAATCTTTTGTCAATAGAGCCAGGAC 1053
QY 241 LeuIleHisGlnLeuLeuArgArgAseProAlaAseArgLeuSerLeuSerValLeu 260
DB 1054 CTTATTCACAGTTACTTCTGTTAGAAATCCAGCAGATCGTTTAAAGTCTGTTCTCAGTATG 1113
QY 261 AspHisProPheMetSerArgAseSerSerThrLysSerLysAsePheLeuGlyThrValGlu 280
DB 1114 GACCATCTTTTATGTTCCCGAAATTTCTTCAACAAAAAGTAAAGATTAGGAACCTGGAA 1173
QY 281 AseSerIleAseSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerSerThr 300
DB 1174 GACTCAATTTGATAGTGGGCATGCCAATTTCTACTGCAATTTACAGCTTCTTCCAGTACC 1233
QY 301 SerIleSerGlySerLeuPheAseLysArgArgLeuLeuIleGlyGlnProLeuProAse 320
DB 1234 AGTATAAGTGGTAGTTTATTTGACAAAAAGAGACTTTTGAATTTGGTTCGCCACTCCCAAT 1293
QY 321 LysMetThrValPheProLysAseLysSerSerThrAsePheSerSerSerSerGlyAspGly 340
DB 1294 AAAATGACTGTTATTTCCAAAGATAAAAGTTCACTGATTTTCTTCTTCAGGAGATGGA 1353
QY 341 AseSerPheTyThrGlnTrpGlyAseGlnGlnThrSerAseSerGlyArgGlyArgVal 360
DB 1354 AACAGTTTTTATCTACTGTTGGGAAATCAAGAAACAGTAAATAGTGGAGGAGAGATA 1413
QY 361 IleGlnAseAlaGluGluArgProHisSerArgTyLeuArgArgAlaTySerSerAse 380
DB 1414 ATTCAGATGTCAGAAAGAAAGGCCATTTCTCGATACCTTCGTAGAGCTTATTTCTCTCAT 1473

381 ArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArgCysHis 400
1474 AGATCTGGCAGCTTCTAATAGTCAGTCTCAAGCAAAACATATACAAATGGAACGATGTCAC 1533
401 SerAlaGluMetLeuSerValSerLysArgSerGlyGlyGlyGluAsnGluGluArgTyr 420
1534 TCAGCAGAAATGCTTTCAGTCTCCAAAGATCAGGAGGAGGTGAATAAGAGAGAGGTAC 1593
421 SerProThrAspAsnAlaAsnIlePheAsnPhePheLysGluLysThrSerSerSer 440
1594 TCACCACACAGACAACATGCCAACATTTTAACTCTTTTAAAGAAAAGACATCCAGTAGT 1653
441 SerGlySerPheGluArgProAspAsnGlnAlaLeuSerAsnHisLeuCysProGly 460
1654 TCTGGATCTTTTGAAGAGCCTCATTAACAATCAAGCACTCTCCAATCATCTTTGTCCAGGA 1713
461 LysThrProPheProPheAlaAspProThrProGlnThrGluThrValGlnGlnTrpPhe 480
1714 AAAACTCTCTTTTCCATTTGCAGACCCGACACTTCAGACTGAACCCGTACACAGTGGTTT 1773
481 GlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrThrGluTyrAspSerIleSerPro 500
1774 GGGAAATCTGCAATAAATGCTCATTTAAGAAAAAATCTACTGAATATGACAGCATCAGCCCA 1833
501 AsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLysAsnAlaTrpThr 520
1834 AACCGGAGCTTCAGGGCCATCCAGATTTGCAAGAGGACACATCAAAAAAATGCCGACT 1893
521 AspThrLysValLysLysAsnSerAspAlaSerAspAsnAlaHisSerValLysGlnGln 540
1894 GATACAAAAGTCAAAAGAACTCTGATGCTTCTGATATGACATCTCTGTAACACGAA 1953
541 AsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleIleGlnGluCys 560
1954 AATACCATGAAATATATGACTGCACCTTCACAGTAAACCTGAGATAATCAACAAGATGT 2013
561 ValPheGlySerAspProLeuSerGluGlnSerLysThrArgGlyMetGluProTrp 580
2014 GTTTTGGCTCAGATCCTCTTCTGAACAGACAGACACTAGGGGTATGGAGCCACCATGG 2073
581 GlyTyrGlnAsnArgThrLeuArgSerIleThrSerProLeuValAlaHisArgLeuLys 600
2074 GGTATCAGAAATCGTACATTAGAGCATTATCTCCGTTGGTGTCTCAGAGTTAATA 2133
601 ProIleArgGlnLysThrLysLysAlaValValSerIleLeuAspSerGluGluValCys 620
2134 CCAATCAGACAGAAAAACCAAAAGGCTGTGGTGAGCATACTTGTATTCAGAGGAGGTGT 2193
621 ValGluLeuValLysGluTyrAlaSerGlnGluTyrValLysGluValLeuGlnIleSer 640
2194 GTGGAGCTTGTAAAGGAGTATGCATCTCAAGAAATATGTGAAGAAAGTTCTTCAGATATCT 2253
641 SerAspGlyAsnThrIleThrIleTyrTyrProAsnGlyGlyArgGlyPheProLeuAla 660
2254 AGTGATGAAAACGATCATCTATTATATCCAAATGGTGGTAGAGTTTCTCTGTCT 2313
661 AspArgProProSerProThrAspAsnIleSerArgTyrSerPheAspAsnLeuProGlu 680
2314 GATAGACCCCTCCTACTGACACATCAGTAGGTACAGCTTTGACAAATTTACAGAA 2373
681 LysTyrTrpArgLysTyrGlnTyrAlaSerArgPheValGlnLeuValArgSerLysSer 700
2374 AAATCTGGCGAAAAATCAATATGCTTCCAGGTTTGTACAGCTTGTAAAGATCTAAATCT 2433
701 ProLysIleThrTyrPheThrArgTyrAlaLysCysIleLeuMetGluAsnSerProGly 720
2434 CCCAAATCACTATTTTACAGATATGCTAAATGCAATTTTATGAGAGATTTCTCTGT 2493
721 AlaAspPheGluValTrpPheTyrAspGlyValLysIleHisLysThrGluAspPheIle 740
2494 GCTGATTTTGGGTTTGGTTTATGATGGGTAAAAATACACAAAACAGAGATTTTCAT 2553
741 GlnValIleGluLysThrGlyLysSerTyrThrLeuLysSerGluSerGluValAsnSer 760

Db 2554 CAGGTGATTGAAAAGACAGGGAAGTCTTACACTTTTAAAAAGTGAAGTAAATAGC 2613
Qy 761 LeuLysGluGluIleLysMetTyrMetAspHisAlaAsnGluGlyHisArgIleCysLeu 780
Db 2614 TTGAAGAGGAGATAAAAATGATATGACCATCTAATGAGGTCATCGTATTGTTTA 2673
Qy 781 AlaLeuGluSerIleLysSerGluGluArgLysThrArgSerAlaProPhePhePro 800
Db 2674 GCACCTGGAATCCATAATTTTCAAGAGAGAAAGGAAAACTAGGAGTGTCTCCCTTTTCCCA 2733
Qy 801 IleIleIleGlyArgLysProGlySerThrSerSerProLysAlaLeuSerProPro 820
Db 2734 ATAATCATAGGAAGAAACCTGGTAGTACTAGTTTCACTAAGGGCTTATACCTCTCTCT 2793
Qy 821 SerValAspSerAsnTyrProThrArgAspArgAlaSerPheAsnArgMetValMetHis 840
Db 2794 TCTGTGGATTCAAATTTACCCAAACGAGAGATAGAGCACTTTTCAACAGAAATGTCATGCAT 2853
Qy 841 SerAlaAlaSerProThrGlnAlaProIleLeuAsnProSerMetValThrAsnGluGly 860
Db 2854 AGTGTGCTTCTCCAAACACAGGCCCAATCCTTAATCCCTCTATGTTTACAAATGAAGGA 2913
Qy 861 LeuGlyLeuThrThrThrAlaSerGlyThrAspIleSerSerAsnSerLeuLysAspCys 880
Db 2914 CTTGTGCTCTTCAACTCAGACTTCTGGAAACAGACATCTCTCTAATAGTCTAAAAAGATTGT 2973
Qy 881 LeuProLysSerAlaGlnLeuLeuLysSerValPheValLysAsnValGlyTrpAlaThr 900
Db 2974 CTTCTTAATCAGACACAACCTTTTGAATCTGTTTTTGTGAANAATGTTGGTTGGCTACA 3033
Qy 901 GlnLeuThrSerGlyAlaValTrpValGlnPheAsnAspGlySerGlnLeuValGln 920
Db 3034 CAGTTAACTAGTGAGCTGTGTGGTTCAGTTTAAATGATGGGTCCAGTTGGTTGTGCAG 3093
Qy 921 AlaGlyValSerSerIleSerTyrThrSerProAsnGlyGlnThrArgTyrGlyGlu 940
Db 3094 GCAGGAGTGTCTTATCAGTTATACCTTCAACAAATGGTCAACAACTAGGTATGGAGAA 3153
Qy 941 AsnGluLysLeuProAspTyrIleLysGlnLysLeuGlnCysLeuSerSerIleLeuLeu 960
Db 3154 AATGAAAAATTCACAGACTACATCAACAGAAATTCAGTGTCTGTCTTCCATCTTTTG 3213
Qy 961 MetPheSerAsnProThrProAsnPheHis 970
Db 3214 ATGTTTCTAATCCGACTCCTTAATTTTCAT 3243

RESULT 4

US-10-116-802-108

; Sequence 108, Application US/10116802

; Publication No. US20030065157A1

; GENERAL INFORMATION:

; APPLICANT: Amy Lasek

; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER

; FILE REFERENCE: PA-0045 US

; CURRENT APPLICATION NUMBER: US/10/116,802

; PENDING FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: 60/281,593

; PRIOR FILING DATE: 2001-04-04

; NUMBER OF SEQ ID NOS: 519

; SOFTWARE: PERL Program

; SEQ ID NO 108

; LENGTH: 3721

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No: 492750CB1

US-10-116-802-108

Alignment Scores:

Pred. No.: 0

Score: 5071.00

Length:

Matches:

3721

968

Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	99.79%	Mismatches:	0
Query Match:	99.86%	Indels:	0
DB:	14	Gaps:	0
US-10-026-021-2 (1-970) x US-10-116-802-108 (1-3721)			
QY	1	MetAlaThrCysIleGlyGluIysIleGluAspPheLysValGlyAsnLeuLeuGlyLys	20
DB	288	ATGGCCACCTGTCATCGGGGAGAGATCGAGGATTTTAAAGTTGGAATCTGCTTGGTAA	347
QY	21	GlySerPheAlaGlyValTyrArgAlaGluSerIleHisThrClyLeuGluValAlaIle	40
DB	348	GGATCAATTTGCTGTCTACAGAGCTGAGTCCATTCACACTGGTTTGAAGTTGCAATC	407
QY	41	LysMetIleAspLysLysAlaMetTyrLysAlaGlyMetValGlnArgValGlnAsnGlu	60
DB	408	AAATGATAGATAAGAAAGCCATGTACAAAGCAGGATGTTACAGAGTCAAAATGAG	467
QY	61	ValLysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu	80
DB	468	GTGAAATACATTCGCAATTGAAACATCTCTATCTTGGAGCTTTATTAATATTITGAA	527
QY	81	AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyClnuMetAsnArgTyr	100
DB	528	GATAGCAATTTATGTGTATCTGGTATTAGAAATGTCCATAATGGAGAAATGAACAGGTAT	587
QY	101	LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle	120
DB	588	CTAAGATAGAGTGNAAACCTTCTCAGAAATGAAGCTCGACACTTCATGACACAGATC	647
QY	121	IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer	140
DB	648	ATCAGAGGATGTGTATCTTCATCTCATGTGTATACACCGGACCTCACACTTCT	707
QY	141	AsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGln	160
DB	708	AACTCTCTACTGACTCGTAATATGAACATCAAGATTTGCTGATTTGGCCCTGGCAACTCAA	767
QY	161	LeuLysMetProHisGlyLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPro	180
DB	768	CTGAAATGCCACATGAAAGACATATACATTTATGTGGAACTCTTAACTACATTTACCA	827
QY	181	GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTyrSerLeuGlyCysMet	200
DB	828	GAAATTTGCCACTCGAAGTGCACATGCGCTTTGAATCTGATGTTGGTCCCTGGCTGTATG	887
QY	201	PheTyrThrLeuLeuIleGlyArgProProPheAspThrAspThrValLysAsnThrLeu	220
DB	888	TTTTATACATTTATATCGGGAGACCACCTTCGACACTGCACAGTCAAGAACACATTA	947
QY	221	AsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAsp	240
DB	948	AATAAGTAGTAGTTCGACATTTATGAAATGCCAACTTTTTTGTCAATAGAGGCCAAGGAC	1007
QY	241	LeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerValLeu	260
DB	1008	CTTATTCACAGTACTTCTGTAGAAATCCAGCAGATCGTTTAAAGTCTGTCTTCAGTATTTG	1067
QY	261	AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu	280
DB	1068	GACCATCTCTTTATGTCTCCGAAATCTTCAACAAAGATAAGATTTAGGAACCTGTGGAA	1127
QY	281	AspSerIleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerSerThr	300
DB	1128	GACTCAATTTGATGGGCGATGCCCAATTTCTACTGCAATTTACAGCTTTCTCCAGTACC	1187
QY	301	SerIleSerGlySerLeuPheAspLysArgArgLeuLeuIleGlyClnProLeuProAsn	320
DB	1188	AGTATAAGTGTAGTTTATTTGACAAAGAGACTTTTGTATTTGGTCAGCCACTTCCAAAT	1247
QY	321	LysMetThrValPheProLysAsnLysSerSerThrAspPheSerSerSerGlyAspGly	340

DB	1248	AAAATGACTGTATTTTCCAAAGAAATAAAAGTTTCAACTGATTTTTTCTTCTTCCAGGATGGA	1307
QY	341	AsnSerPheTyrThrGlnTyrGlyAsnGlnGluThrSerAsnSerGlyArgGlyVal	360
DB	1308	AACAGTTTTTATCTCAGTGGGGAATCAAGAAACAGATATAGTGGAAAGGAGATTA	1367
QY	361	IleGlnAspAlaGluGluArgProHisSerArgTyrLeuArgArgAlaTyrSerSerAsp	380
DB	1368	ATTCAAGATGCAGAAAGAAAGGCCACATTTCTCGATACCTTCGTAGAGCTTATTTCTCTGAT	1427
QY	381	ArgSerGlyThrSerAsnSerClnSerGlnAlaLysThrTyrMetClnuArgCysHis	400
DB	1428	AGATCTGGCACTTCTAATAGTCACTCAAGCAAAACATATACAAATGGAACGATGTAC	1487
QY	401	SerAlaGluMetLeuSerValSerLysArgSerGlyGlyGlyLysGlnGluArgTyr	420
DB	1488	TCAGCAGAAATGCTTTTCAAGTGTCCAAAGATCAAGAGAGGTGAAATGAAGAGGTAC	1547
QY	421	SerProThrAspAsnAsnAlaAsnIlePheAsnPheLysGlyLysThrSerSerSer	440
DB	1548	TCACCCACAGACAACAATGCCAACATTTTAACTTCTTTAAAGAAAGACATCCAGTAGT	1607
QY	441	SerGlySerPheGluArgProAspAsnAsnGlnAlaLeuSerAsnHisLeuCysProGly	460
DB	1608	TCTGGATCTTTTGAAGACCTGATAACAATCAAGCACTCTCCAATCATCTTTGTCCAGGA	1667
QY	461	LysThrProPhePheAlaAspProThrProGlnThrGluThrValGlnGlnTyrPhe	480
DB	1668	AAACTCTTTTCCATTTTGCAGACCCGACCTCAGACTGAAACCGTACACAGTGGTTT	1727
QY	481	GlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrGluTyrAspSerIleSerPro	500
DB	1728	GGGAATCTGCAAAATAAATGCTCATTTAAGAAAACTACTGTAATATGACAGCATCAGCCA	1787
QY	501	AsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLysAsnAlaTyrThr	520
DB	1788	AACGGGACTTCCAGGGCCATCCAGATTTGAGAGAGGACACATCAAAAAATGCTGGACT	1847
QY	521	AspThrLysValLysLysAsnSerAspAlaSerAspAsnAlaHisSerValLysGlnGln	540
DB	1848	GATACAAAGTCAAAAAGAACTCTGATGCTTCTGATAATGCACATCTCTGTAAGACGAA	1907
QY	541	AsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleIleGlnGlnCys	560
DB	1908	AATACATGAAATATATGACTGCATTCACAGTAAACCTGAGATAATCCACACAGATGT	1967
QY	561	ValPheGlySerAspProLeuSerGlnSerLysThrArgGlyMetGluProProTyr	580
DB	1968	GTTTTGGCTCAGATCTCTTTCTGAAACAGAGCAAGACTAGGGGTATGGAGCCACATGG	2027
QY	581	GlyTyrGlnAsnArgThrLeuArgSerIleThrSerProLeuValAlaHisArgLeuLys	600
DB	2028	GGTTATCAGATCGTACATTAAGAACATTCATCTCCGTTGGTTGCTCACAGGTTAAAA	2087
QY	601	ProIleArgGlnLysThrLysLysAlaValValSerIleLeuAspSerGluGluValCys	620
DB	2088	CCAATCAGACAGAAAAACCAAAAGGCTGTGGTGAGCATACTTGTATTCAGAGAGGTGTCT	2147
QY	621	ValGluLeuValLysGluTyrAlaSerGlnGluTyrValLysGluValLeuGlnIleSer	640
DB	2148	GTGGAGCTGTGAAAGGAGTATGATCTCAAGATATGTGAAAGAAAGTTCTTTCAGATATCT	2207
QY	641	SerAspGlyAsnThrIleThrIleTyrTyrProAsnGlyGlyArgGlyPheProLeuAla	660
DB	2208	AGTGATGAAATACGATCACTATTATTATCCAAATGGTGTAGAGGTTTCTCTTCTCT	2267
QY	661	AspArgProProSerProThrAspAsnIleSerArgTyrSerPheAspAsnLeuProGlu	680
DB	2268	GATAGACACCCCTCACCTACTGACAAACATCAGTAGGTACAGCTTTTGACATTTACCAGA	2327
QY	681	LysTyrTyrArgLysTyrGlnTyrAlaSerArgPheValGlnLeuValArgSerLysSer	700
DB	2328	AAATACTGGCGAAATATCAATATGCTTCCAGGTTTGTACAGCTTGTGAAGATCTAAATCT	2387

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QY 701 ProLysIleThrThrPheThrArgTyrAlaLysCysIleLeuMetGluAsnSerProGly 720
Db 2388 CCCAAATCACCATTATTTTACAGATATGCTAAATGTCATTTTATGAGAGATTTCTCTGCT 2447
QY 721 AlaAspPheGluValTyrPheTyrAspGlyValLysIleHisLeuThrGluAspPheIle 740
Db 2448 GCTGATTTGAGTTTGGTTTATGATGGGGTAAATACAAACAGAGATTTCATT 2507
QY 741 GlnValIleGluLysThrGlyLysSerTyrThrLeuLysSerGluSerGluValAsnSer 760
Db 2508 CAGGTGATTTGAAAGACAGCGAAGTCTTACACTTTTAAAAAGTGAAGTGAAGTTAATAGC 2567
QY 761 LeuLysGluGluIleLysMetTyrMetAspHisAlaAsnGluGlyHisArgIleCysLeu 780
Db 2568 TTGAAAGAGAGATAAAAATGATATGGACCATGCTAATGAGGGTCATCGTATTTGTTTA 2627
QY 781 AlaLeuGluSerIleIleSerGluGluArgLysThrArgSerAlaProPhePro 800
Db 2628 GCACGTGAATCCATATTTTCAGAGAGGAAAGAAACCTAGAGGTGCTCCCTTTTCCCA 2687
QY 801 IleIleIleGlyArgLysProGlySerThrSerProLysAlaLeuSerProPro 820
Db 2688 ATAATCATAGGAAGAAACCTGGTAGTACTAGTTCACCTAAGGCTTATCACCTCCTCT 2747
QY 821 SerValAspSerAsnTyrProThrArgAspArgAlaSerPheAsnArgMetValMetHis 840
Db 2748 TCTGTGGATTTCAAATTTACCAACGAGAGATAGAGCATCTTTCAACAGAAATGGTCATGCAT 2807
QY 841 SerAlaAlaSerProThrGlnAlaProIleLeuAsnProSerMetValThrAsnGluGly 860
Db 2808 AGTGCTGCTTCTCCAAACAGGACCAATCCCTTATCCCTCTATGTTTACAAATGAAGA 2867
QY 861 LeuGlyLeuThrThrAlaSerGlyThrAspIleSerSerAsnSerLeuLysAspCys 880
Db 2868 CTTGGTCTTTACAACTACAGCTTCTGGAACAGACATCTCTTCTAATAGTCTAAAGATTGT 2927
QY 881 LeuProLysSerAlaGlnLeuLysSerValPheValLysAsnValGlyTyrAlaThr 900
Db 2928 CTTCTTAATACAGCAACTTTGAAATCTGTTTTTGTGAAAAATGTTGGTTGGGCTACA 2987
QY 901 GlnLeuThrSerGlyValaValTyrValGlnPheAsnAspGlySerGlnLeuValGln 920
Db 2988 CAGTTAACTAGTGGAGCTGTGGTTCAGTTTAAATGATGGTCCAGTTGGTTGGCAG 3047
QY 921 AlaGlyValSerSerIleSerTyrThrSerProAsnGlyGlnThrThrArgTyrGlyGlu 940
Db 3048 GCAGGAGTGCTTCTATCATCAGTTATACCTCACCAAATGGTCAAACTAGGTATGGAGAA 3107
QY 941 AsnGluLysLeuProAspTyrIleLysGlnLysLeuGlnCysLeuSerSerIleLeuLeu 960
Db 3108 AATGAAAAATTACAGACTACATCAACAGAAATTACAGTGTCTGTCTTCCATCCTTTTG 3167
QY 961 MetPheSerAsnProThrProAsnPheHis 970
Db 3168 ATGTTTCTTAATCCGACTCCTAATTTTCAT 3197
RESULT 5
US-10-737-450-89
; Sequence 89, Application US/10737450
; Publication No. US20040235071A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Ecsedy, Jeffrey A.
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tighe Nestor, Michelle
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 15986, 2188, 20743, 9148, 9151, 9791, 44252,
; TITLE OF INVENTION: 14184, 42467, 8204, 7970, 25552, 21657, 26492, 2411, 15088,
; TITLE OF INVENTION: 1905, 28899, 63380, 33935, 10480, 12686, 25501, 17694,
; TITLE OF INVENTION: 15701, 53062, 49908, 21612, 38949, 6216, 46863, 9235, 2201,
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; TITLE OF INVENTION: 6985, 9883, 12238, 18057, 21617, 39228, 49928, 54476, 62113,
; TITLE OF INVENTION: 64316, 12264, 32362, 58198, 2887, 3205, 8557, 9600, 9693,
; TITLE OF INVENTION: 44867, 53058, 55556, 57658, 2208, 10252, 10302, 14218,
; TITLE OF INVENTION: 33877, 10317, 10485, 25964, 14815, 1363, 1397, 14827, 21708,
; TITLE OF INVENTION: 3803, 64698, 2179 OR 13249
; FILE REFERENCE: MPI02-207P1RNMNIM
; CURRENT APPLICATION NUMBER: US/10/737,450
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/435,108
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/436,443
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/438,498
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/444,370
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/446,031
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: US 60/453,635
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/457,199
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/462,458
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/466,732
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/469,184
; PRIOR FILING DATE: 2003-05-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 3092
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (141)... (3053)
US-10-737-450-89
Alignment Scores:
Pred. No.: 0 Length: 3092
Score: 5067.00 Matches: 967
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 99.69% Mismatches: 0
Query Match: 99.78% Indels: 0
DB: 20 Gaps: 0
US-10-026-021-2 (1-970) x US-10-737-450-89 (1-3092)
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QY 21 GlySerPheAlaGlyValTyrArgAlaGluSerIleHisThrGlyLeuGluValaIle 40
Db 201 GGATCATTTGCTGTGTCTACAGAGCTGAGTCCATTCACACTGGTTTGGAAAGTTGCAATC 260
QY 41 LysMetIleAspLysLysAlaMetTyrLysAlaGlyMetValGlnArgValGlnAsnGlu 60
Db 261 AAAATGATAGTAAAGAAAGCCATGTACAAACAGAGATGGTACAGAGAGTCAAAAATGAG 320
QY 61 VallysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu 80
Db 321 GTGAAAAATACATTGCCAATTCGAAACATCTCTATCTTGGAGCTTTATATACTATTTTGA 380
QY 81 AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyr 100
Db 381 GATAGCAATTTATGTATCTGTTATGAAATATGCCAATATGGAGAAATGAACAGGTAT 440
QY 101 LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle 120
Db 441 CTAAAGATAGAGTGAACCCCTTCTCGAAATGAAGCTCGACACTTCATTCACACAGATC 500
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121 IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer 140
501 ATCACAGGATGTTGATCTTCACTCTCATGTGTATACACCGGACCTCACACTTCT 560
141 AsnLeuLeuThrArgAsnMetAsnIleLysIleAlaAspGlyLeuAlaThrGln 160
561 AACCTCCCTACTACTCGTAAATATGAACATCAAGATTGCTGATTTTGGGCTGGCACTCAA 620
161 LeuLysMetProHisGluLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPro 180
621 CTGAAATGCCACATGAAAGACATATACATTTATGTGTGACCTTCACTACATTTTCAACA 680
181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTyrSerLeuGlyCysMet 200
681 GAAATTTGCCCTCGAAGTGCACATGGCTTGAATCTGATGTTTGGTCCCTGGGCTGTATG 740
201 PheTyrThrLeuLeuIleGlyArgProProPheAspThrAspThrValLysAsnThrLeu 220
741 TTTTATACATTACTTATCGGGAGACCCCTTCGACACTGCACACAGTCAAGAACACATTA 800
221 AsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAsp 240
801 AATAAGTAGTATTGGCAGATTATGAATGCCACCTTTTGTCTCAATAGAGGCCCAAGAC 860
241 LeuIleHisGlnLeuLeuArgAsnProAlaAspArgLeuSerLeuSerSerValLeu 260
861 CTTATTACCACTTACTTCGTAGAAATCCAGCAGATCGTTTAAGTCTGTCTTCAGTATTG 920
261 AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu 280
921 GACCATCTCTTTATGTCGCCGAAATTTCTCAACAAAAGTAAAGATTTAGGAACCTGGAA 980
281 AspSerIleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerSerThr 300
981 GACTCAATTGATGTTGGGATGCCCAATTTCTACTGCAATTACAGCTTCTTCCAGTACC 1040
301 SerIleSerGlySerLeuPheAspLysArgArgLeuLeuIleGlyGlnProLeuProAsn 320
1041 AGTATAAGTGGTAGTTTATTGACAAAAGAGACATTTTGAATGGTCAGCCACTCCCAAT 1100
321 LysMetThrValPheProLysAsnLysSerSerThrAspPheSerSerSerGlyAspGly 340
1101 AAAATGACTGTATTTTCCAAAGAAATAAAAGTTCAACTGATTTTCTCTTCAGGAGATGGA 1160
341 AsnSerPheTyrThrGlnTyrGlyAsnGlnGluThrSerAsnSerGlyArgGlyVal 360
1161 AACAGTTTTATCTCAGTGGGGAAATCAAGAAACCCAGTAATAGTGGGAAGGGGAAGAGTA 1220
361 IleGlnAspAlaGluArgProHisSerArgTyrLeuArgArgAlaTyrSerSerAsp 380
1221 ATTCAGATGCGAAGAAAGGCCACATTTCTCGATACCTTCGTAGAGCTTATCTCTGAT 1280
381 ArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArgCysHis 400
1281 AGATCTGGCACTTCTAATAGTCAGTCTCAAGCAAAACATATACAAATGGAACGATGTAC 1340
401 SerAlaGluMetLeuSerValSerLysArgSerGlyGlyGlyAsnGluArgTyr 420
1341 TCAGCAGAAATGCTTTTCAGTGTCCAAAAGATCAGGAGGAGGTGAAAATGGAAGAGAGTAC 1400
421 SerProThrAspAsnAlaAsnIlePheAsnPheLysGluLysThrSerSerSer 440
1401 TCACCCACAGACAAACATGCCAACATTTTAACTTCTTTAAAGAAAAGACATCCAGTAGT 1460
441 SerGlySerPheGluArgProAspAsnAsnGlnAlaLeuSerAsnHisLeuSerProGly 460
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461 LysThrProPheProPheAlaAspProThrProGlnThrGluThrValGlnGlnTyrPhe 480
1521 AAAACTCTCTTTTCCATTTTGCAGACCCGACACCTCAGACTGAAACCGGTACAAACAGTGGTTT 1580

481 GlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrThrGluTyrAspSerIleSerPro 500
1581 GGGAACTCTGCAAAATAAATGCTCAITTTAAGAAAACTACTGAATATGACAGCATCAGCCCA 1640
501 AsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLysAsnAlaTyrThr 520
1641 AACCGGACTTCCAGGGCCCATCCAGATTGAGAAAGGACACATCAAAAAAATGCTCGACT 1700
521 AspThrLysValLysLysAsnSerAspAlaSerAspAsnAlaHisSerValLysGlnGln 540
1701 GATACAAAGTCAAAAGAAACTCTGATGCTTCTGATAATGACATCTCTGTAACACGCA 1760
541 AsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleIleGlnGlnGluCys 560
1761 AATACCATGAATATATGACTGCATTCACAGTAAACCTGAGATAATCCAAACAAGATCT 1820
561 ValPheGlySerAspProLeuSerGluGlnSerLysThrArgGlyMetGluProProTyr 580
1821 GTTTTGGCTCAGATCCTCTTCTGAACAGAGCAAGACTAGGGGTATGGGCCACCATGG 1880
581 GlyTyrGlnAsnArgThrLeuArgSerIleThrSerProLeuValAlaHisArgLeuLys 600
1881 GGTATCAGATCGTACATTAAAGACATTAATCTCCGTTGGTGTCTCAGAGTTAAA 1940
601 ProIleArgGlnLysThrLysLysAlaValValSerIleLeuAspSerGluGluValCys 620
1941 CCAATCAGACAGAAAAACCAAAAGGCTGTGTGAGCATACTTGTATTCAGAGGAGGTGT 2000
621 ValGluLeuValLysGluTyrAlaSerGlnGluTyrValLysGluValLeuGlnIleSer 640
2001 GTGGAGCTTGTAAAGGAGTATGCATCTCAAGAAATATGTGAAGAAAGTTCTTTCAGATATCT 2060
641 SerAspGlyAsnThrIleThrIleTyrTyrProAsnGlyGlyArgGlyPheProLeuAla 660
2061 AGTGAATGAATACATCATCTATTTATTCAAATGGTGTGTAGAGGTTTCTCTCTTGTCT 2120
661 AspArgProProSerProThrAspAsnIleSerArgTyrSerPheAspAsnLeuProGlu 680
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681 LysTyrTyrArgLysTyrGlnTyrAlaSerArgPheValGlnLeuValArgSerLysSer 700
2181 AAATACTGGCGAAAATATCAATATGCTTCCAGGTTTGTACAGCTTGTAAAGATCTAAATCT 2240
701 ProLysIleThrTyrPheThrArgTyrAlaLysCysIleLeuMetGluAsnSerProGly 720
2241 CCAAAATCACTTATTTTACAGATATGCTAAATGCTATTTTGTAGGGAAATCTCTCTGT 2300
721 AlaAspPheGluValTyrPheTyrAspGlyValLysIleHisLysThrGluAspPheIle 740
2301 GCTGATTTTGGGTTTGGTTTATGATGGGTAAAATATACACAAAACAGAGATTTTCAT 2360
741 GlnValIleGluLysThrGlyLysSerTyrThrLeuLysSerGluSerGluValAsnSer 760
2361 CAGTGATTTGAAAAGACAGGGAAGTCTTACACTTTAAAAAGTGAAGTAAATAGC 2420
761 LeuLysGluGluIleLysMetTyrMetAspHisAlaAsnGluGlyHisArgIleCysLeu 780
2421 TTGAAAGAGGAGATAAAAATGTTTATGGACCATGCTAATAGGGGTCACTGATTTTGT 2480
781 AlaLeuGluSerIleIleSerGluGluArgLysThrArgSerAlaProPhePhePro 800
2481 GCATCGNAATCCATATTTTCAAGAGAGAAAGAACTAGAGTGTCTCCCTTTTCCCA 2540
801 IleIleIleGlyArgLysProGlySerThrSerProLysAlaLeuSerProProPro 820
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2601 TCTGTGATTTCAAAATTTACCAACAGAGATAGAGCATCTTTTCAACAGAAATGGTTCATG 2660
841 SerAlaAspProThrGlnAlaProIleLeuAsnProSerMetValThrAsnGluGly 860

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Db      2661 AGTGCTGCTCTCCAAACAGCAGCCCAATCCTTAATCCTCTATGTTACAAATCAAGGA 2720
Qy      861 LeuGlyLeuThrThrAlaSerGlyThrAspIleSerSerAsnSerLeuLysAspCys 880
Db      2721 CTTGGTCTTACAACTACAGCTTCTCGAACAGACATCTCTCTTAATAGTCTAAAGATTGT 2780
Qy      881 LeuProLysSerAlaGlnLeuLeuLysSerValPheValLysAsnValGlyTrpAlaThr 900
Db      2781 CTTCTTAATACGACAACTTTGAAATCTGTTTGTGAAATAATGTTGGTTGGGCTACA 2840
Qy      901 GlnLeuThrSerGlyValaValTrpValGlnPheAsnAspGlySerGlnLeuValGln 920
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Qy      921 AlaGlyValSerSerIleSerTyrThrSerProAsnGlyGlnThrThrArgTyrGlyGlu 940
Db      2901 GCAGGAGTGTCTCTATCAGTTATACCTCACCAATGGTCAAAACAATAGGTATGGAGAA 2960
Qy      941 AsnGluLysLeuProAspTyrIleLysGlnLysLeuGlnCysLeuSerSerIleLeuLeu 960
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Qy      961 MetPheSerAsnProThrProAsnPheHis 970
Db      3021 ATGTTTCTTAATCCGACTCCTTAATTTTCAT 3050

RESULT 6
US-10-887-553A-750
; Sequence 750, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; with insulin signalling dysregulation
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; PRIOR FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 750
; LENGTH: 3331
; TYPE: DNA
; ORGANISM: human
US-10-887-553A-750

Alignment Scores:
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Score: 5057.00 Matches: 965
Percent Similarity: 99.79% Conservative: 3
Best Local Similarity: 99.48% Mismatches: 2
Query Match: 99.59% Indels: 0
DB: 21 Gaps: 0

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Qy      21 GlySerPheAlaGlyValTyrArgAlaGluSerIleHisThrGlyLeuGluValAlaIle 40
Db      249 GGATCATTTGCTGGTGTCTACAGAGCTGAGTCCATTCACAGTGGTTTGGAAAGTTGCAATC 308
Qy      41 LysMetIleAspLysIleAlaMetTyrLysAlaGlyMetValGlnArgValGlnAsnGlu 60
Db      309 AAAATGATAGATAGAAAGCCCATGATACAAAGCAGGAATGGTACAGAGAGTCCAAATGAG 368
Qy      61 ValLysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGlu 80
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Db      369 GTGAAATACATTCGCAATTTGAAACATCCTTCTATCTTTGGAGCTTTATAACTATTTTGAA 428
Qy      81 AspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyr 100
Db      429 GATAGCAATATATGTTATCTGTTATAGAAATGTGCCATAATGGGAGAAATGAACAGGTAT 488
Qy      101 LeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle 120
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Qy      121 IleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSer 140
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Qy      141 AsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGln 160
Db      609 AACCTCCTACTGACTCGTAAATATGAACATCAAGATTGCTGATTTTGGCTGGCAACTCAA 668
Qy      161 LeuLysMetProHisGluLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPro 180
Db      669 CTGAAATGCCACATGAAAGCACTATACATATTGTGGAACCTCTTAATACATTTTACCA 728
Qy      181 GluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTrpSerLeuGlyCysMet 200
Db      729 GAAATTGCCACTCGAAGTGCACATGGCTTGAATCTGATGTTTGGTCCCTGGGCTGTATG 788
Qy      201 PheTyrThrLeuLeuIleGlyArgProPheAspThrAspThrValLysAsnThrLeu 220
Db      789 TTTTATACATTACTATCGGGAGACCACCCCTTCGACACTGCACAGTCAAGAACACATTA 848
Qy      221 AsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAsp 240
Db      849 AATAAAGTAGTATTGGCAGATTATGAAATGCCAATCTTTTGTCAATAGAGGCCAAGGAC 908
Qy      241 LeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerSerValLeu 260
Db      909 CTTATTCACCAGTTACTTCGTAGAAATCCAGCAGATCGTTTAAGTCTGCTTTCAGTATTG 968
Qy      261 AspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGlu 280
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Qy      301 SerIleSerGlySerLeuPheAspLysArgArgLeuLeuIleGlyGlnProLeuProAsn 320
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Qy      341 AsnSerPheTyrThrGlnTrpGlyAsnGlnGluThrSerAsnSerGlyArgGlyArgVal 360
Db      1209 AACAGTTTTTATCTCAGTGGGGAAATCAAGAAACCCAGTAATAGTAGGGGGAAGAGTA 1268
Qy      361 IleGlnAspAlaGluGluArgProHisSerArgTyrLeuArgArgAlaTyrSerSerAsp 380
Db      1269 ATTCAGATGTCAGAAAGAAAGGCCACATTTCTCGATACCTTTCGTAGAGCTTATTTCTCTGAT 1328
Qy      381 ArgSerGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArgCysHis 400
Db      1329 AGATCTGGCACTTCTAATAGACAGTCTCAAGCAAAAAACATATACAATGAACAGATGTCCAC 1388
Qy      401 SerAlaGluMetLeuSerValSerLysArgSerGlyGlyGlyGluAsnGluGluArgTyr 420
Db      1389 TCACAGAAATGCTTTTCAGTGTCCAAAGATCAGAGGAGGTGAAATATAGAGAGGATAC 1448
Qy      421 SerProThrAspAsnAsnAlaAsnIlePheAsnPhePheLysGluLysThrSerSerSer 440
Db      1449 TCACCCACAGACAAACAATGCCAACATTTTAACTTTTAAAGAAAAAGACATCCAGTAGT 1508
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QY 461 LysThrProPheProPheAlaAspProThrProGlnThrGluThrValGlnGlnTrpPhe 480
DB 1569 AAAACTCTCTTTCCATTTTGCAGACCCGACCACTCAGACTGAACCGTACACAGTGGTTT 1628
QY 481 GlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrThrGluTyAspSerIleSerPro 500
DB 1629 GGGATCTGCAAAATAAATGCTCATTTAAGAAAAAATCTACTGAATATGACAGCATCAGCCCA 1688
QY 501 AsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLysAsnAlaTrpThr 520
DB 1689 AACCGGAGCTTCAGGGCCATCCAGATTTGCAGAAAGGACACATCAAAAAATGCCGTGACT 1748
QY 521 AspThrLysValLysLysAsnSerAspAlaSerAspAsnAlaHisSerValLysGlnGln 540
DB 1749 GATACAAAAGTCAAAAGAACTCTGATGCTTCTGATAATGCAATCTCTGTAAACAGCAAA 1808
QY 541 AsnThrMetLysThrMetThrAlaLeuHisSerLysProGluIleLeuGlnGlnCys 560
DB 1809 AATACCATGAATATATGACTGCATCTCACAGTAAACCTGAGATTAATCCACACAGATGT 1868
QY 561 ValPheGlySerAspProLeuSerGluGlnSerLysThrArgGlyMetGluProTrp 580
DB 1869 GTTTTGGCTCAGATCTCTTCTGAAACAGAGCAAGACTAGGGGTATGGAGCCACCATGG 1928
QY 581 GlyTyGlnAsnArgThrLeuArgSerIleThrSerProLeuValAlaHisArgLeuLys 600
DB 1929 GGTATATCAAGATCGTACATTAAGAGCAATATACATCTCCGTTGGTTGCTCACAGGTAAATA 1988
QY 601 ProfileArgGlnLysThrLysLysAlaValValSerIleLeuAspSerGluGluValCys 620
DB 1989 CCAATCAGACAGAAACCAAAAGGCTGTGTGACATATCTTGATTCAGAGGAGGTGTGT 2048
QY 621 ValGluLeuValLysGluTyTrpAlaSerGlnGluTyValLysGluValLeuGlnIleSer 640
DB 2049 GTGGAGCTGTGAAGAGATGATGCATCTCAAGAATATGTGAAGAAGTCTTCCAGATATCT 2108
QY 641 SerAspGlyAsnThrIleThrIleTyTrpProAsnGlyGlyArgGlyPheProLeuAla 660
DB 2109 AGTGATGAAATACCATCATCTATTTATTTATTCATAATGGTGGTGGTGGTGGTGGTGGT 2168
QY 661 AspArgProProSerProThrAspAsnIleSerArgTyTrpSerPheAspAsnLeuProGlu 680
DB 2169 GATAGACCACTCTACCTACTGACAAATCATGATGATGATGATGATGATGATGATGATGATG 2228
QY 681 LysTyTrpArgLysTyTrpGlnTyTrpAlaSerArgPheValGlnLeuValArgSerLysSer 700
DB 2229 AAATACTGGCGAAATATCAATATGCTTCCAGGTTTGTACAGCTTCTAAGATCTAAATCT 2288
QY 701 ProLysIleThrTyTrpPheThrArgTyTrpAlaLysCysIleLeuMetGluAsnSerProGly 720
DB 2289 CCCAAATCACTTATTTTACAGATATGCTAAATGCAATTTTGTATGAGGATCTCTCTGGT 2348
QY 721 AlaAspPheGluValTrpPheTyTrpAspGlyValLysIleHisLysThrGluAspPheIle 740
DB 2349 GCTGATTTTGGGTTTGGTTTATGATGGGGTAAATAATACAAACAGAGATTTTCATT 2408
QY 741 GlnValIleGluLysThrGlyLysSerTyTrpThrLeuLysSerGluSerGluValAsnSer 760
DB 2409 CAGGTGATGTAAGACAGAGGAGTCTTACACTTTTAAAGTGAAGTGAAGTGAAGTGAAGT 2468
QY 761 LeuLysGluGluIleLysMetTyTrpMetAspHisAlaAsnGluGlyHisArgIleCysLeu 780
DB 2469 TTGAAAGAGGAGATAAATGATGATGACCATGCTAATGAGGTCATCGTATTGTTTA 2528
QY 781 AlaLeuGluSerIleIleSerGluGluArgLysThrArgSerAlaProPhePro 800
DB 2529 GCATGGGAATCCATAATTTCAAGAGAGGAAAGGAAACCTAGGAGTGCCTCCCTTTTCCCA 2588

QY 801 IleIleIleGlyArgLysProGlySerThrSerSerProLysAlaLeuSerProPro 820
DB 2589 ATAATCATAGGAAGAAAAACCTGGTAGTACTAGTTCCACCTTAAGGCCTTATCACCTCTCT 2648
QY 821 SerValAspSerAsnTyTrpThrArgAspArgAlaSerPheAsnArgMetValMetHis 840
DB 2649 TCTGTGGATTCAAAATTTACCAACGAGATGAGCATCTTTTCAACAGAAATGGTCAATGCAT 2708
QY 841 SerAlaAlaSerProThrGlnAlaProIleLeuAsnProSerMetValThrAsnGluGly 860
DB 2709 AGTGATGCTTCTCCAAACACAGGCACCAATCCTTAATCCTCTATGTTTACAAATGAAGA 2768
QY 861 LeuGlyLeuThrThrAlaSerGlyThrAspIleSerSerAsnSerLeuLysAspCys 880
DB 2769 CTTGGTCTTCAAACTACAGCTTCTGAAACAGACATCTCTTCTAATAGTCTAAAGATTGT 2828
QY 881 LeuProLysSerAlaGlnLeuLysSerValPheValLysAsnValGlyTrpAlaThr 900
DB 2829 CTTCTTAATCAGACAACTTTTGAAATCTGTTTTTGAAAAATGTTGGTTGGGCTACA 2888
QY 901 GlnLeuThrSerGlyValAlaValTrpValGlnPheAsnAspGlySerGlnLeuValValGln 920
DB 2889 CAGTTAACTAGTGGAGCTGTGTGGGTTCAAGTTTAATGATGGTCCAGTGGTGTGGAG 2948
QY 921 AlaGlyValSerSerIleSerTyTrpThrSerProAsnGlyGlnThrArgTyGlyGlu 940
DB 2949 GCAGAGTGTCTCTATCAGTTATACCTCACCAATGGTCAAAACAACTAGGTATGGAGAA 3008
QY 941 AsnGluLysLeuProAspTyTrpIleLysGlnLysLeuGlnCysLeuSerSerIleLeuLeu 960
DB 3009 AATGAAATAATTTACCAGACTACATCAACAGAAATTTACAGTGTCTGTCTTCCATCTTTTG 3068
QY 961 MetPheSerAsnProThrProAsnPheHis 970
DB 3069 ATGTTTCTAATCCGACTCTTAATTTTCAT 3098
RESULT 7
US-10-425-114-26254
; Sequence 26254, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26254
; LENGTH: 2836
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-112-B4_FLI
US-10-425-114-26254
Alignment Scores:
Pred. No.: 0 Length: 2836
Score: 4861.00 Matches: 927
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.89% Mismatches: 0
Query Match: 95.73% Indels: 0
DB: 18 Gaps: 0
US-10-026-021-2 (1-970) x US-10-425-114-26254 (1-2836)
QY 43 IleAspTyLysAlaMetTyTrpLysAlaGlyMetValGlnArgValGlnAsnGluValLys 62

Db 2 ATAGATAGAAAGCCATGTCAAAACAGGAATGGTACAGAGTCCAAAATGAGGTGAA 61
Qy 63 IleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGluAspSer 82
Db 62 ATACATTGCCAATTGAACATCCTTCTATCTTGGAGCTTATAACTATTTTGAAGATAGC 121
Qy 83 AsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyrLeuLys 102
Db 122 AATTATGTGTATCTCGTATTTAGAAATGTGCCAATAATGGAGAAATGAA CAGGTATCTAAAG 181
Qy 103 AsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIleIleThr 122
Db 182 AATAGAGTGAAACCTTCTCAGAAAATGAAGCTCGACACTTCATGCACCAGATCATACA 241
Qy 123 GlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSerAsnLeu 142
Db 242 GGGATGTTGTATCTTCAATCTCATGGTATATACACCGGAGCCTCACACTTCTTAACCTC 301
Qy 143 LeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGlnLeuLys 162
Db 302 CTACTGACTCGTAAATATGAACATCAAGATTTGCTGATTTTGGCTGGCAACTCAACTGAAA 361
Qy 163 MetProHisGluLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerProGluIle 182
Db 362 ATGCCACATGAAAGCAGCTATATATGTGGAACTCTTAACACTACATTTCCACGAAAT 421
Qy 183 AlaThrArgSerAlaHisGlyLeuGluSerAspValTyrPheLeuGlyCysMetPheTyr 202
Db 422 GCCACTGAAAGTGACATGGCCCTTGAATCTGATGTTGGTCCCTGGGCTGATGTTTAT 481
Qy 203 ThrLeuLeuIleGlyArgProPheAspThrValLysAsnThrLeuAsnLys 222
Db 482 ACATTACTTATCGGAGAGCCACCTTCGACACTGCACAGTCAAGCAAGAACACATTAATAAA 541
Qy 223 ValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAspLeuIle 242
Db 542 GTAGTATTGGCAGATTGAATGCCATCTTTTGTCAATAGAGGCCAAGGACCTTAT 601
Qy 243 HisGlnLeuLeuArgAsnProAlaAspArgLeuSerLeuSerSerValIleAspHis 262
Db 602 CACCAAGTTACTTTCGTAGAAATCCAGCAGATCGTTTAAAGTCTGTCTTCAGTATTGGACCAT 661
Qy 263 ProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGluAspSer 282
Db 662 CTTTTTATGTCCCGAAATCTTCAACAAAAGTAAGATTTAGGAACCTGTGGAAGACTCA 721
Qy 283 IleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerSerThrSerIle 302
Db 722 ATTTGATGTGGCATGCCACAATTTCTACTGCAATTCACAGCTTCTTCCAGTACCAGTATA 781
Qy 303 SerGlySerLeuPheAspLysArgArgLeuLeuIleGlyGlnProLeuProAsnLysMet 322
Db 782 AGTGTAGTATTATTTGACAAAAGAAAGACTTTTGAATGGTTCAGCCACTCCCAAAATAAAATG 841
Qy 323 ThrValPheProLysAsnLysSerSerThrAspPheSerSerSerGlyAspGlyAsnSer 342
Db 842 ACTGATTTCCAAAGAAATAAAGTTCAACTGATTTTCTTCTTCAGGAGATGGAAACAGT 901
Qy 343 PheTyrThrGlnTrpGlyAsnGlnGluThrSerAsnSerSerGlyArgValIleGln 362
Db 902 TTTTATACTCAGTGGGAAATCAAGAACCCAGTAAATAGTGGAGGGGAGAGTAAATCAA 961
Qy 363 AspAlaGluGluArgProHisSerArgTyrLeuArgAlaTyrSerSerAspArgSer 382
Db 962 GATGCAGAAAGAAAGGCCAATTTCTCGATACCTTCGTAGAGCTTATTCCTCTGATAGATCT 1021
Qy 383 GlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArgCysHisSerAla 402
Db 1022 GGCACCTTCTAATAGTCAGTCTCAAGCAAAAACATATACAATGGAACGATGTCACTCAGA 1081
Qy 403 GluMetLeuSerValSerLysArgSerGlyGlyGlyGluAsnGluGluArgTyrSerPro 422
Db 1082 GAAATGCTTTTCAAGTTCACAAAAGATCAGGAGGAGGTGAAATGAAGAGAGGTACTCACCC 1141

Qy 423 ThrAspAsnAsnAlaAsnIlePheAsnPhePheLysGluLysThrSerSerSerSerGly 442
Db 1142 ACAGACAACAATGCCAACTTTTAACTTCTTTAAAGAAAGACATCCAGTAGTTCTGGA 1201
Qy 443 SerPheGluArgProAspAsnAsnGlnAlaLeuSerAsnHisLeuCysProGlyLysThr 462
Db 1202 TCTTTTGAAGACCTGATTAACAATCAAGCACTCTCCAATCATCTTTGTCCAGGAAAAC 1261
Qy 463 ProPheProPheAlaAspProThrProGlnThrGluThrValGlnGlnTrpPheGlyAsn 482
Db 1262 CCTTTTCCATTTGTCAGACCCGACACCTCAGACTGAAACCGTACAACAGTGGTTGGGAAT 1321
Qy 483 LeuGlnIleAsnAlaHisLeuArgLysThrThrGluTyrAspSerIleSerProAsnArg 502
Db 1322 CTGCAATAAATGCTCATCTTTAAGAAAAAACTACTGAATATGACAGCATCAGCCCAACCG 1381
Qy 503 AspPheGlnGlyHisProAspLeuGlnLysAspThrSerLysAsnAlaTyrThrAspThr 522
Db 1382 GACTTCCAGGCCCATCCAGATTTGCAGAGGACACATCAAAAAATGCTCGACTGATACA 1441
Qy 523 LysValLysLysAsnSerAspAlaSerAspAsnAlaHisSerValLysGlnGlnAsnThr 542
Db 1442 AAAGTCAAAAAGAACTCTGATGCTTCTGATAATGSCACATCTCTGTAACACAGCAATACC 1501
Qy 543 MetLysTyrMetThrAlaLeuHisSerLysProGluIleLeuGlnGlnGluCysValPhe 562
Db 1502 ATGAAATATATGACTGCACCTTACAGTAAACCTGAGATAATCCAAACAAGATGTGT 1561
Qy 563 GlySerAspProLeuSerGluGlnSerLysThrArgGlyMetGluProTrpGlyTyr 582
Db 1562 GGCTCAGATCTCTTCTGAAACAGCAAGACTAGGGGTATGGAGCCACCATTGGGTTAT 1621
Qy 583 GlnAsnArgThrLeuArgSerIleThrSerProLeuValAlaHisArgLeuLysProIle 602
Db 1622 CAGAACTGATTAAGAGCATTTACATCTCCGTGGTGGTGCACAGGTTAAAAACCAATC 1681
Qy 603 ArgGlnLysThrLysLysAlaValSerIleLeuAspSerGluGluValCysValGlu 622
Db 1682 AGACAGAAAAACCAAAAGGCTGTGTGAGCATCTTGAATTCAGAGAGGTTGTGTGGAG 1741
Qy 623 LeuValLysGluTyrAlaSerGlnGluTyrValLysGluValLeuGlnIleSerSerAsp 642
Db 1742 CTGTGTAAGGATGATGATCTCAAGAAATATGTGAAGAGTTCTTCAGATATCTAGTGAT 1801
Qy 643 GlyAsnThrIleThrIleTyrTyrProAsnGlyGlyArgGlyPheProLeuAlaAspArg 662
Db 1802 GGAATAACGATCACTATTTATATCCAAATGGTGGTAGAGGTTTCTCTTGTGTGATAGA 1861
Qy 663 ProProSerProThrAspAsnIleSerArgTyrSerPheAspAsnLeuProGluLysTyr 682
Db 1862 CCACCTCACCCTACTCAACATCAGTAGGTACAGCTTTTGACAAATTTTCCAGAAAAATAC 1921
Qy 683 TrpArgLysTyrGlnTyrAlaSerArgPheValGlnLeuValArgSerLysSerProLys 702
Db 1922 TGGCGAAAATATCAATATGCTTCCAGGTTGTACAGCTTGTAAAGATCTAAATCTCCCAA 1981
Qy 703 IleThrTyrPheThrArgTyrAlaLysCysIleLeuMetGluAsnSerProGlyAlaAsp 722
Db 1982 ATCACTTATTTTCAAGATATGCTAAATGCAATTTGATGGAGAATTTCTCTGCTGCTGAT 2041
Qy 723 PheGluValTrpPheTyrAspGlyValLysIleHisLysThrGluAspPheIleGlnVal 742
Db 2042 TTTGAGGTTTGGTTTTATGATGGGGTAAAAATACAAAAACAGAAAGATTTTCATTCAGGTG 2101
Qy 743 IleGluLysThrGlyLysSerTyrThrLeuLysSerGluSerGluValAsnSerLeuLys 762
Db 2102 ATTGAAAAGACAGGGAAGTCTTACACTTTAAAAAGTGAAGTGAAGTTAATAGCTTGAA 2161
Qy 763 GluGluIleLysMetTyrMetAspHisAlaAsnGluGlyHisArgIleCysLeuAlaLeu 782
Db 2162 GAGGAGATAAAAATGATATGAGCACCTGCTAATGAGGCTCATCGTATTTGTTAGCACTG 2221

QY 783 GluSerIleSerGluGluArgLysThrArgSerAlaProPhePheProIlelle 802
Db 2222 GAATCCATAATTTCAAGAGAGAAAGAAATAGGAGTGTCCCTTTTCCCAATATC 2281
QY 803 IleGlyArgLysProGlySerThrSerProLysAlaLeuSerProProSerVal 822
Db 2282 ATAGAAGAAACCTGGTAGTACTAGTTCCACCTAAGGCCCTTATCACCTCTCTCTG 2341
QY 823 AspSerAsnTyrProThrArgAspArgAlaSerPheAsnArgMetValMethHisSerAla 842
Db 2342 GATTCAATATCCCAACGAGAGAGAGAGATCTTTCAACAGAAATGGTCATGATAGTGT 2401
QY 843 AlaSerProThrGlnAlaProIleLeuAsnProSerMetValThrAsnGluGlyLeuGly 862
Db 2402 GCTTCTCCAAACAGAGACCAATCCTTAATCCCTCTATGGTTACAAATGAAGACTTGT 2461
QY 863 LeuThrThrAlaSerGlyThrAspIleSerSerAsnSerLeuLysAspCysLeuPro 882
Db 2462 CTATCAACTACAGCTTCTGGAAACAGACATCTCTTAATAGTCTAAAGATTTGTCTCT 2521
QY 883 LysSerAlaGlnLeuLeuLysSerValPheValLysAsnValGlyTriAlaThrGlnLeu 902
Db 2522 AAATCAGACACTTTTGAATCTGTTTTGTGAAATAATGTTGGTGGCTACACAGTTA 2581
QY 903 ThrSerGlyAlaValTrrpValGlnPheAsnAspGlySerGlnLeuValGlnAlaGly 922
Db 2582 ACTAGTGAGCTGTGTGGGTTTCAATGATGGTCCAGTTCAGTTGGTGGCAGCAGGA 2641
QY 923 ValSerSerIleSerTyrThrSerProAsnGlyGlnThrThrArgTyrGlyGluAsnGlu 942
Db 2642 GTGTCTTCTATCAGTTATACCTCCCAATGGTCAACCAACTAGATATGGAGAAATGAA 2701
QY 943 LysLeuProAspTyrIleLysGlnLysLeuGlnCysLeuSerSerIleLeuLeuMetPhe 962
Db 2702 AAATACCGACTACTACATCAACAGAAATACAGTGTCTGTCTTCCATCTTTTGAATTT 2761
QY 963 SerAsnProThrProAsnPheHis 970
Db 2762 TCTAATCCGACTCCTTAATTTTTCAT 2785

RESULT 8

US-10-062-674-1868
; Sequence 1868, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 1868
; LENGTH: 3924
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040005559A1 332518.2
US-10-062-674-1868

Alignment Scores:

Pred. No.:	0	Length:	3924
Score:	4777.50	Matches:	954
Percent Similarity:	97.16%	Conservative:	5
Best Local Similarity:	96.66%	Mismatches:	11
Query Match:	94.08%	Indels:	17
DB:	17	Gaps:	3

US-10-026-021-2 (1-970) x US-10-062-674-1868 (1-3924)

QY 1 MetAlaThrCysIleGlyGluLysIleGluAspPheLysValGlyAsnLeuLeuGlyLys 20
Db 289 ATGGCGACTGCATCGGGGAGAGATCGAGATTTTAAAGTTGGAAATCTGCTTGTAAA 348
QY 21 GlySerPheAlaGlyValTyrArgAlaGluSerIleHisThrGlyLeuGluValAlaIle 40
Db 349 GGATCATTTGCTGGTGTCTACAGAGCTGAGTCCATTCACTGGTGTGGAAATTCGAATC 408
QY 41 -LysMetIleAspLysLysAlaMetTyrLysAlaGlyMetValGlnArgValGlnAsnGln 60
Db 409 CAAATGATGATAGTAAGAAAGCCATGTCAAGCAGAAATGGTACAGAGATCCAAATGA 468
QY 60 uValLysIleHisCysGlnLeuLysHisProSerIleLeuGluLeuTyrAsnTyrPheGln 80
Db 469 GGTGAAATACATTTGCCAATTTGAAACATCTTCTATCTTGGAGTTTTTATAACTATTTTGA 528
QY 80 uAspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsnGlyGluMetAsnArgTyr 100
Db 529 AGATAGCAATTTATGTGTATCTGGTATTAGAAATGTGCCAATATGGAGAAATGAGCAGGTA 588
QY 100 rLeuLysAsnArgValLysProPheSerGluAsnGluAlaArgHisPheMetHisGlnIle 120
Db 589 TCTAAGAAATAGAGTAAACCTTCTCAGAAATAGAACTGCACACTTCATGCACACAGAT 648
QY 120 eIleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHisArgAspLeuThrLeuSe 140
Db 649 CATCAGAGGATTTGTATCTTCTATCTCATGGTATATACACCGGGACCTCACACTTTC 708
QY 140 rAsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAspPheGlyLeuAlaThrGln 160
Db 709 TAACCTCTACTGACTCGTAAATATGAAACATCAAGATTCGTGATTTGGGTGGCAACTCA 768
QY 160 nLeuLysMetProHisGluLysHisTyrThrLeuCysGlyThrProAsnTyrIleSerPr 180
Db 769 ACTGAAATGCCCATGAAAGACACTATACATTTATGTGGAATCTCTAACTACATTTTACC 828
QY 180 oGluIleAlaThrArgSerAlaHisGlyLeuGluSerAspValTrrpSerLeuGlyCysMe 200
Db 829 AGAAATTCGCACTCGAAGTGCACATGGCTTGAATCTCATGTTGGTCCCTGGGTGTAT 888
QY 200 tPheTyrThrLeuLeuIleGlyArgProPheAspThrAspThrValLysAsnThrIle 220
Db 889 GTTTTATACATTAATCTATCGGGAGACCACTTTCGACACTGCACAGTCAAGAACACAT 948
QY 220 uAsnLysValValLeuAlaAspTyrGluMetProSerPheLeuSerIleGluAlaLysAs 240
Db 949 AAATAAAGTAGTATTGGCAGATTATGAAATGCCAATCTTTTGTCAATAGAGGCCAAGA 1008
QY 240 pLeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeuSerLeuSerSerValle 260
Db 1009 CTTTATTCACAGTTACTTCGTAGAAATCCAGCAGATCGTTTAACTGTCTTCAAGTATT 1068
QY 260 uAspHisProPheMetSerArgAsnSerSerThrLysSerLysAspLeuGlyThrValGln 280
Db 1069 GGACCATCTTTTATGTCCGAAATTTCTCAACAAAAAGTAAAGATTAGGAATCTGTGA 1128
QY 280 uAspSerIleAspSerGlyHisAlaThrIleSerThrAlaIleThrAlaSerSerSerTh 300
Db 1129 AGACTCAATGATAGTGGGCATGCCAATTTCTACTGCAATATACAGTCTTCTTCAGTAC 1188
QY 300 rSerIleSerGlySerLeuPheAspLysArgArgLeuLeuIleGlyGlnProLeuProAs 320
Db 1189 CAGTATAAGTGTAGTTTATTTGACAAAGAAAGACTTTTGTGTCAGCCACTCCCAA 1248
QY 320 nLysMetThrValPheProLysAsnLysSerSerThrAspPheSerSerSerGlyAspGln 340
Db 1249 TAAATGACTGTATTTCCAAAGATAAAAGTTCAACTGATTTTCTTCTTCAGGAGATGG 1308
QY 340 yAsnSerPheTyrThrGlnTrrpGlyAsnGlnGluThrSerAsnSerGlyArgGlyArgVa 360
Db 1309 AAACAGTTTTTATCTACTGCTGGGAAATCAAGAAACCAAGTAAATAGTGAAGGGGAGAGT 1368
QY 360 lIleGlnAspAlaGluGluArgProHisSerArgTyrLeuArgAlaTyrSerSerAs 380

Db 1369 AATTCAAGATGCAGAGAAAGCCACATTCCTCGATACCTTCGTAGAGCTTATTCCTCTGA 1428
QY 380 pARserGlyThrSerAsnSerGlnSerGlnAlaLysThrTyrThrMetGluArgCysHi 400
Db 1429 TAGATCTGGCACTTCTAATAGTTCAGTCTCAAGCAAAAACATATACAATGGAACGATGTCA 1488
QY 400 sSerAlaGluMetLeuSerValSerIysArgSerGlyGlyGlyGluAsnGluGluArgTy 420
Db 1489 CTCAGAGAAATGCTTTTCAGTGTCCAAAGATCAGAGAGGTGAAATGAAGAGAGGTA 1548
QY 420 rSerProThrAspAsnAsnAlaAsnIlePheAsnPhePheLysGluLysThrSerSerSe 440
Db 1549 CTCACCCACAGACAACATGCCCAATTTTAACTTCTTTAAAGAAAAGACATCCAGTAG 1608
QY 440 rSerGlySerPheGluArgProAspAsnAsnGlnAlaLeuSerAsn-HisLeuCysProG 460
Db 1609 TTCTGGATCTTTTGAAGACCTGATAACAATCAAGCACTCTCCAATGCATCTTTGTCCAG 1668
QY 460 lYlYsThrProPheProPheAlaAspProThrProGlnThrClnuThrValGlnGlnTrpP 480
Db 1669 GAAAAACTCTCTTTCCATTTGAGACCCGACACCTCAGACTGAAACCGTACAACACAGTGGT 1728
QY 480 heGlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrThrGluTyrzAspSerIleSerP 500
Db 1729 TTGGGAATCTGCAATTAATGCTCATTTAAGAAAACACTACTGAATATGACAGCATCAGCC 1788
QY 500 roAsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLysAsnAlaTrpT 520
Db 1789 CAAACCGGACCTTCAGGGCCCATCCAGATTTTCAGAAAGACACATCAAAAAATGCTGGA 1848
QY 520 hrAspThrIysValLysLysAsnSerAspAlaSerAspAsnAlaHisSerValLysGlnG 540
Db 1849 CTGATACAAAAGTCAAAAAGAACTCTGATGCTTCTGATAATGCACATTTCTGTAAACACG 1908
QY 540 InAsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleLeuGlnGlnGluC 560
Db 1909 AAAATACCATGAAATATATGACTGCACCTTCACAGTAAACCTGAGATATATCCAAAGAA 1968
QY 560 ySValPheGlySerAspProLeuSerGluGlnSerLysThrArgGlyMetGluProProT 580
Db 1969 GTGTGTTTTGGCTTCAGATCTCTTTCTGAACAGACGCAAGACTAGGGGTATGAGCCACCAT 2028
QY 580 rGlyTyrGlnAsnArgThrLeuArgSerIleThrSerProLeuValAlaHisArgLeuL 600
Db 2029 GGGGTATCAGAAATCGTACATTAAGAAGCATTTACATCTCCGTTGGTGTCTCACAGGTTAA 2088
QY 600 ySProIleArgGlnLysThrLysLysAlaValValSerIleLeuAspSerGluGluValC 620
Db 2089 AACCAATCAGACAGAAACCAAAAAGGCTGTGGTGAGCATACTTGAATTCAGAGGAGGTGT 2148
QY 620 ySValGluLeuValLysGluTyrAlaSerGlnGluTyrValLysGluValLeuGlnIleS 640
Db 2149 GTGTGGAGCTTGAAGGAGTATGATCTCAAGAATATGTGAAGAAAGTCTTCAGATAT 2208
QY 640 erSerAspGlyAsnThrIleThrIleTyrTyrProAsnGly-GlyArgGlyPheProLeu 659
Db 2209 CTAGTGATGGAATACGATCACTATTATTTATCCAAATGGTGGGTAGAGGTTTCCCTCTT 2268
QY 660 Ala-AspArgProProSerProThr-AspAsnIleSerArgTyrSerPheAspAsnLeuP 679
Db 2269 GCTGTAGTAGACACCTCACCTACTTGTGACACATCAGTAGGTACAGCTTTGACAAATTTAC 2328
QY 679 roGluLysTyrTrpArgLysTyrGlnTyrAlaSerArgPheValGlnLeuValArgSerL 699
Db 2329 CAGAAAAATACCTGGCGAAAAATATCAATATGCTTCCAGGTTTGTACAGCTTGTGAAGATCTA 2388
QY 699 ySerSerProLysIleThrTyrPheThrArgTyrAlaLysCysIleLeuMetGluAsnSerP 719
Db 2389 AATCTCCCAAAATCACTTATTTTCAAGATATGCTAAATGCAATTTGTAGTGAGAAATCTC 2448
QY 719 roGlyAlaAspPheGluValTrpPheTyrAspGlyValLysIleHisLysThrGluAspP 739

Db 2449 CTGTGCTGATTTTGGAGTTTGGTTTATGATGGGTAAAAATACAAAAACAGAGATT 2508
QY 739 heIleGlnValIleGluLysThrGlyLysSerTyrThrLeuLysSerGluSerGluVala 759
Db 2509 TCATTCCAGTGATTTGAAAAGACAGGAAGTCTTACACTTTAAAAAGTGAAGTTA 2568
QY 759 snSerLeuLysGluGluIleLysMetTyr-MetAspHisAlaAsn-GluGlyHisArgI 778
Db 2569 ATAGCTTGAAGAGAGAGATAAAAAATGTATAATGGACCATGTCTAATGGAGGGTCACTGAT 2628
QY 778 eCysLeuAlaLeuGluSerIleLeSerGluGluGluArgLysThrArgSerAlaProPh 798
Db 2629 TTGTTTACCACTGGAAATCCATAATTTCAGAGAGAGAAAGAAACTAGAGGTGCTCCCTT 2688
QY 798 ePheProIleIleLeGlyArgLysProGly-SerThrSerSerProLysAlaLeuSerP 818
Db 2689 TTTCCCAATAATCATAGGAAGAAACCTGTTGAGTACTAGTTTCCACTAAGGCTTTATCAC 2748
QY 818 roProProSer-ValAspSerAsnTyrProThrArgAspArgAlaSerPheAsnArgMet 837
Db 2749 CTCCTCTCTTCTTGTGGATTTCAAAATTTACCCAACGAGAGATAGAGCATCTTTCAACAGAATG 2808
QY 838 ValMethHisSerAlaAlaSerProThrGlnAlaProIleLeuAsnProSerMetValThr 857
Db 2809 GTCATGCATAGTGTCTTCTCCAACACAGGACCAATCCTTAATCCCTCTATGGTTACA 2868
QY 858 AsnGluGlyLeuGlyLeuThrThrAlaSerGlyThr-AspIleSerSerAsnSerLe 877
Db 2869 AATGAAGACCTTGGTCTTACAACTACAGGTTTGGGACGACATCTCTTCTAATAGTCT 2928
QY 877 uLysAspCysLeuPro---LysSerAlaGlnLeuLysSer-ValPheValLysAsn- 895
Db 2929 AAAAGATGTCTTCTCTATAATCACGACCACTTTTGAATCTCGTTTTGTGAAAAAT 2988
QY 896 --ValGlyTrpAla---ThrGlnLeuThrSerGlyAlaValTrpValGlnPheAsnAspG 914
Db 2989 GTTTGGTTGGGCATACCACCACTTAAGTGTGGGCTGTGGGTTAGTTTAAATGATG 3048
QY 914 lySerGlnLeuValValGlnAla-GlyValSerSer-IleSerTyrThrSerProAsnG 933
Db 3049 GGTCCTCAGTTGGTGTGCGAGGACAGAGTGTCTTCAACAAGTTATACCTCACCAGATG 3108
QY 933 yGlnThr-ThrArgTyrGlyGluAsnGluLysLeuProAspTyrIleLysGlnLysLeuG 953
Db 3109 TCAAAACCACTAGTATATGGAGAAATGAAAAATTTACCGGACTACATCAACAGAAATTAC 3168
QY 953 InCysLeuSerSerIleLeuLeuMetPheSerAsnProThrProAsnPheHis 970
Db 3169 AGTGTCTGTCTCCATCTTTTGATGTTTCTAATCCGACTTCTTAATTTTTCAT 3221

RESULT 9

US-09-918-995-21560
; Sequence 21560, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIORITY FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21560
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(484)
; OTHER INFORMATION: n = A,T,C or G

US-09-918-995-21560

Alignment Scores:

Pred. No.: 2,26e-61 Length: 484
Score: 743.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.63% Indels: 0
DB: 10 Gaps: 0

US-10-026-021-2 (1-970) x US-09-918-995-21560 (1-484)

Qy 676 AsnAlaTrpThrPheGlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrGluTyrAsp 695
Db 59 GACAAATTTACAGAAAATACTGGCGAAAATATCAATATGCTTCAGGTTTGTACAGCTT 118
Qy 696 ValArgSerLysSerProLysIleThrTyrPheThrArgTyrAlaLysCysIleLeuMet 715
Db 119 GTAAGATCTAATCTCCCAAAATCACTATTTTACAGATATGCTTAATGCAATTTTGTATG 178
Qy 716 GluAsnSerProGlyAlaAspPheGluValTrpPheTyrAspGlyValLysIleHisLys 735
Db 179 GAGAATCTCTGCTGCTGATTTTGAGGTTTGTATGATGGGTAATAAATACACAAA 238
Qy 736 ThrGluAspPheIleGlnValIleGluLysThrGlyLysSerTyrThrLeuLysSerGlu 755
Db 239 ACAGAAGATTTCAATTCAGGTGATTCGAAAGACAGCGAAGTCTTACACTTTTAAAAAGTGAA 298
Qy 756 SerGluValAsnSerLeuLysGluLysIleLysMetTyrMetAspHisAlaAsnGluGly 775
Db 299 AGTGAAGTTATAGCTTGAAGAGAGAGATAAAATGATATGACCATCTGCTTAATGAGGGT 358
Qy 776 HisArgIleCysLeuAlaLeuGluSerIleLeuSerGluGluGluArgLysThrArgSer 795
Db 359 CATCGTATTTCTTAGCACTGGAATCCATATTTTCAGAGAGAGAAAGAACTAGGAGT 418
Qy 796 AlaProPhePheProIleIleIleGlyArgLysProGlySerThrSerSerProLysAla 815
Db 419 GCTCCCTTTTCCCAATAATCATAGGAAGAAAACCTGCTAGTACTAGTTACCTAAGGCC 478
Qy 816 LeuSer 817
Db 479 TTATCA 484

RESULT 10

US-09-878-178-96
; Sequence 96, Application US/09878178
; Patent No. US2002017552A1

GENERAL INFORMATION:

; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secretist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527
; CURRENT APPLICATION NUMBER: US/09/878,178
; NUMBER OF SEQ ID NOS: 2337
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 328
; TYPE: DNA
; ORGANISM: Homo sapien

US-09-878-178-96

Alignment Scores:

Pred. No.: 2,44e-47 Length: 328
Score: 594.00 Matches: 109
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.70% Indels: 0
DB: 9 Gaps: 0

US-10-026-021-2 (1-970) x US-09-878-178-96 (1-328)

Qy 477 GlnGlnTrpPheGlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrGluTyrAsp 496
Db 2 CAACAGTGGTTTGGGAATCTGCAATAAATGCTCATTTAAGAAAACTACTGAATATGAC 61
Qy 497 SerIleSerProAsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLys 516
Db 62 AGCATCAGCCCAACCCGGGACTTCAGGGCCATCCAGATTTTGCAGAGAGACACATCAAAA 121
Qy 517 AsnAlaTrpThrAspThrLysValLysValAsnSerAspAlaSerAspAsnAlaHisSer 536
Db 122 AATGCCCTGGACTGATACAAAAGTCAAAAAGAACTCTGATGCTTCTGATATATGCACATTCT 181
Qy 537 ValLysGlnGlnAsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleIle 556
Db 182 GTAAACACAGCAAAATACCATGAATATATGATGCTCACTTTCACAGTAAACCTGAGATAATC 241
Qy 557 GlnGlnGluCysValPheGlySerAspProLeuSerGluGlnSerLysThrArgGlyMet 576
Db 242 CAACAAGAATGTGTTTTTGGCTCAGATCCTCTTTCTGAACACAGAGCAAGACTAGGGGTATG 301
Qy 577 GluProProTrpGlyTyrGlnAsnArg 585
Db 302 GAGCCACCATGGGTTTATCAGAATCGT 328

RESULT 11

US-10-046-935-96

; Sequence 96, Application US/10046935

; Publication No. US2002015601A1

GENERAL INFORMATION:

; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secretist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046,935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2339
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 328
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-046-935-96

Alignment Scores:

Pred. No.: 2,44e-47 Length: 328
Score: 594.00 Matches: 109
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.70% Indels: 0
DB: 13 Gaps: 0

US-10-026-021-2 (1-970) x US-10-046-935-96 (1-328)

Qy 477 GlnGlnTrpPheGlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrGluTyrAsp 496
Db 2 CAACAGTGGTTTGGGAATCTGCAATAAATGCTCATTTAAGAAAACTACTGAATATGAC 61
Qy 497 SerIleSerProAsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLys 516
Db 62 AGCATCAGCCCAACCCGGGACTTCAGGGCCATCCAGATTTTGCAGAGAGACACATCAAAA 121
Qy 517 AsnAlaTrpThrAspThrLysValLysValAsnSerAspAlaSerAspAsnAlaHisSer 536
Db 122 AATGCCCTGGACTGATACAAAAGTCAAAAAGAACTCTGATGCTTCTGATATATGCACATTCT 181
Qy 537 ValLysGlnGlnAsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleIle 556

Db 182 GTAAACAGCAAAATACCATGAATATATGACTGCACTTACAGTAAACCTGAGATAATC 241
QY 557 GlnGlnGluCysValPheGlySerAspProLeuSerGluGlnSerIleThrArgGlyMet 576
Db 242 CAACAGAAGTGTGTTTTGGCTCAGATCCTCTTTCTGAACAGCAAGCAGTAGGGGTATG 301
QY 577 GluProProTrpGlyTyrGlnAsnArg 585
Db 302 GAGCCACCATTGGGTATATCAGAAATCGT 328

RESULT 12

US-10-146-502-96
; Sequence 96, Application US/10146502
; Publication No. US20030069180A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secretist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: AND DIAGNOSIS OF COLON CANCER
; CURRENT APPLICATION NUMBER: US/10/146,502
; CURRENT FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 328
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-502-96

Alignment Scores:
Pred. No.: 2,446-47 Length: 328
Score: 594.00 Matches: 109
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.70% Indels: 0
Gaps: 0

US-10-026-021-2 (1-970) x US-10-146-502-96 (1-328)

QY 477 GlnGlnTrpPheGlyAsnLeuGlnIleAsnAlaHisLeuArgLysThrGluTyrAsp 496
Db 2 CAACAGTGGTTGGGAATCTGCAATAAATGCTCAATTAAGAAAAAATCTGAATATGAC 61
QY 497 SerIleSerProAsnArgAspPheGlnGlyHisProAspLeuGlnLysAspThrSerLys 516
Db 62 AGCATCAGCCCAACACCGGGACTTCCAGGGCCATCCAGATTTCAGAGAAGACACATCAAA 121
QY 517 AsnAlaTrpThrAspThrLysValLysLysAsnSerAspAlaSerAspAsnAlaHisSer 536
Db 122 AATGCTCGACTGTATACAAAAGTCAAAAAGAACTCTGATGCTTCTGATAATGCATTTCT 181
QY 537 ValLysGlnGlnAsnThrMetLysTyrMetThrAlaLeuHisSerLysProGluIleIle 556
Db 182 GTAAACAGCAAAATACCATGAATATATGACTGCACTTCAAGTAAACCTGAGATAATC 241
QY 557 GlnGlnGluCysValPheGlySerAspProLeuSerGluGlnSerLysThrArgGlyMet 576
Db 242 CAACAGAAGTGTGTTTTGGCTCAGATCCTCTTTCTGAACAGCAAGCAGTAGGGGTATG 301
QY 577 GluProProTrpGlyTyrGlnAsnArg 585
Db 302 GAGCCACCATTGGGTATATCAGAAATCGT 328

RESULT 13

US-10-108-580-1
; Sequence 1, Application US/10108580
; Publication No. US20030077681A1
; GENERAL INFORMATION:
; APPLICANT: Cogswell, John

; TITLE OF INVENTION: PLK3 PROTEIN-PROTEIN INTERACTIONS
; FILE REFERENCE: PU4458
; CURRENT APPLICATION NUMBER: US/10/108,580
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (37)..(1860)
; OTHER INFORMATION:
US-10-108-580-1

Alignment Scores:
Pred. No.: 1e-45 Length: 2169
Score: 590.50 Matches: 115
Percent Similarity: 57.33% Conservative: 61
Best Local Similarity: 37.46% Mismatches: 106
Query Match: 11.63% Indels: 25
Gaps: 4

US-10-026-021-2 (1-970) x US-10-108-580-1 (1-2169)

QY 15 GlyAsnLeuLeuGlyLysGlySerPheAlaGlyValTyrArgAlaGluSerIleHisThr 34
Db 112 GGCGCTTGTGGGCAAGGGGGCTTCGCCGCTGCTACGAGGCCACATGACACAGAGACT 171
QY 35 GlyLeuGluValAlaIleLysMetIleAspLysLysAlaMetTyrLysAlaGlyMetVal 54
Db 172 GGCGCGCTACGCTGCAAGTCAATCCGAGAGCGCGTCGCAAGCCCGCATCAGCGC 231
QY 55 GlnArgValGlnAsnGluValLysIleHisCysGlnLeuLysHisProSerIleLeuGlu 74
Db 232 GAGAAGATCTTAATGAGATTGAGCTGCACGAGACCTGCAGACCGCCACATCGTGGCT 291
QY 75 LeuTyrAsnTyrPheGluAspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsn 94
Db 292 TTTTCGACCACCTTTTGGAGCGCTGACAAATCTACATTTCTTGGAGCTCTGCAGCGA 351
QY 95 GlyGluMetAsnArgTyrLeuLysAsnArgValLysProPheSerGluAsnGluAlaArg 114
Db 352 AAGTCCCTGGCCACATCTGGAAGGCCCGG---CACACCCTGTTGGAGCCAGAGTGGCG 408
QY 115 HisPheMetHisGlnIleIleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHis 134
Db 409 TACTACCTGGCGCAGATCTTTCTGGCTCAAGTACTTGCACCGCGCGGCATCTTGAC 468
QY 135 ArgAspLeuThrLeuSerAsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAsp 154
Db 469 CGGACCTCAAGTTGGGAAATTTTTCATCACTCAGAAACATGGAACATGAAGTGGGGAT 528
QY 155 PheGlyLeuAlaThrGlnLeuLysMetProHisGluLysHisTyrThrLeuCysGlyThr 174
Db 529 TTTGGCTGGCGCCCGCGTGGAGCCTCCGAGCAGAGAGAAAGAACCATCTGTGGCACC 588
QY 175 ProAsnTyrIleSerProGluIleAlaThrArgSerAlaHisGlyLeuGluSerAspVal 194
Db 589 CCCAACTATGTGGCTCCAGAGTCTGCTGAGACAGGGCCACGGCCCTGAAGCGGATGTA 648
QY 195 TrpSerLeuGlyCysMetPheTyrThrLeuLeuIleGlyArgProProPheAspThrAsp 214
Db 649 TGGTCACTGGGCTGTGTACATGATACAGCTGCTCTGCGGGAGCCCTCCCTTTGAGACG 708
QY 215 ThrValLysAsnThrLeuAsnLysValLeuAlaAspTyrGluMetProSerPheLeu 234
Db 709 GACCTGAAGGAGACGTACCGCTGCTCAAGCAGAGTTCTACAGCTGCCCTGCCGCTC 768
QY 235 SerIleGluAlaLysAspLeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeu 254
Db 769 TCACTGCTGCCCGCAGCTCTCTGGCGCCATCTCTGGGGCTCTCACCGCCGAGACGCC 828

QY 255 SerLeuSerSerValLeuAspHisProPheMetSerArgAsnSerSerThrLysSerLys 274
115 HisPheMetHisGlnIleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHis 134
Db 829 TCTATTGACCATCTGGCCATGACTTCTTTACCAAG----- 867
QY 275 AspLeuGlyThrValGluAspSerIleAspSerGlyHisAlaThrIleSerThrAlaIle 294
135 ArgAspLeuThrLeuSerAsnLeuThrArgAsnMetAsnIleLysIleAlaAsp 154
Db 868 -----GGCTACACCCCGATCGACTC-----CCTATCAGCAGCTGCGTG 528
QY 295 ThrAlaSerSerThr-----SerIleSerGly 304
155 PheGlyLeuAlaThrGlnLeuLysMetProHisGlnLysHisTyrThrLeuCysGlyThr 174
Db 907 ACAGTCCCGACACCTGACACCCCCCAACCCAGCTAGGAGTCTGTTGGCCAAAGTTACCAAG 588
QY 305 SerLeuPheAspLysArg 311
175 ProAsnTyrIleSerProGluIleAlaThrArgSerAlaHisGlyLeuGluSerAspVal 194
Db 967 AGCCTCTTTGGCAGAAAGAG 987
589 CCCAACTATGTGGCTCCAGAAAGTGTCTGAGACAGGGCCACGGGCCCTGAACGGATGTA 648
214 TTPSerLeuGlyCysMetPheTyrThrLeuLeuIleGlyArgProPheAspThrAsp 214
649 TGGTCACTGGGCTGTGTATGTACACGCTGCTCTCGGGAGGCCCTCTTGTAGACGGGT 708
QY 215 ThrValLysAsnThrLeuAsnLysValValLeuAlaAspTyrGluMetProSerPheLeu 234
709 GACCTGAAGGAGACGTACCGCTGCATCAAGCAGGTTCACTACACGCTGCTGCCACGCTC 768
QY 235 SerIleGluAlaLysAspLeuIleHisGlnLeuLeuArgAsnProAlaAspArgLeu 254
769 TCACTGCTCCCGCAGCTCTCTGGCGCCCTCTCTCGGGCTCACCCTGAGACGCGCCC 828
QY 255 SerLeuSerSerValLeuAspHisProPheMetSerArgAsnSerSerThrLysSerLys 274
829 TCTATTGACCATCTCGCCATGACTTCTTTACCAAG----- 867
QY 275 AspLeuGlyThrValGluAspSerIleAspSerGlyHisAlaThrIleSerThrAlaIle 294
868 -----GGCTACACCCCGATCGACTC-----CCTATCAGCAGCTGCGTG 906
QY 295 ThrAlaSerSerThr-----SerIleSerGly 304
907 ACAGTCCCGACACCTGACACCCCCCAACCCAGCTAGGAGTCTGTTGGCCAAAGTTACCAAG 966
QY 305 SerLeuPheAspLysArg 311
967 AGCCTCTTTGGCAGAAAGAG 987
Db 967 AGCCTCTTTGGCAGAAAGAG 987

RESULT 14
US-10-204-041-15
; Sequence 15, Application US/10204041
; Publication No. US20030176443A1
; GENERAL INFORMATION:
; APPLICANT: STEIN-GERLACH, MATTHIAS
; APPLICANT: SALASSIDIS, KONSTANTINOS
; APPLICANT: BACHER, GERALD
; APPLICANT: MULLER, STEFAN
; TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Pric
; FILE REFERENCE: AXM-007.1P US
; CURRENT FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2001-05-16
; PRIOR FILING DATE: 2001-05-16
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-204-041-15

Alignment Scores:
Pred. No.: 1e-45 Length: 2169
Score: 590.50 Matches: 115
Percent Similarity: 57.33% Conservative: 61
Best Local Similarity: 37.46% Mismatches: 106
Query Match: 11.63% Indels: 25
DB: 16 Gaps: 4

US-10-026-021-2 (1-970) x US-10-204-041-15 (1-2169)

QY 15 GlyAsnLeuLeuGlyLysGlySerPheAlaGlyValTyrArgAlaGluSerIleHisThr 34
115 HisPheMetHisGlnIleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHis 134
Db 112 GCGCCCTGTTGGTGGCAAGGGGGCTTCGCCGCTGCTACGAGCCGCTGACACAGAGACT 171
QY 35 GlyLeuGluValAlaIleLysMetIleAspLysLysAlaMetTyrLysAlaGlyMetVal 54
172 GGCAGCGCTACGCTGTCAAGTCAATCCGACAGCCGCTGCGCCAGCGGATCAGCGC 231
QY 55 GlnArgValGlnAsnGluValLysIleHisCysGlnLeuLysHisProSerIleLeuGlu 74
232 GAGAAGATCTTAATAGATTGAGTGCACCGACCTGCAGCAGCCGACATCTGCGGT 291
QY 75 LeuTyrAsnTyrPheGluAspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsn 94
292 TTTTGGCACCCTTTGAGGACGCTGACAACTACATTTTCTGGAGCTCTGAGCCGA 351
QY 95 GlyGluMetAsnArgTyrLeuLysAsnArgValLysProPheSerGluAsnGluAlaArg 114
352 AAGTCCCTGGCCCAACATCTGGAAGCCCGG---CACACCCCTTTGGAGCCAGAGTGGCG 408

QY 115 HisPheMetHisGlnIleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHis 134
409 TACTACCTGCGGCAGATCTTTTGGCTCAAGTACTTTCACACGAGCGGCTCTTGGCAC 468
QY 135 ArgAspLeuThrLeuSerAsnLeuThrArgAsnMetAsnIleLysIleAlaAsp 154
469 CGGACCTCAAGTTGGGAATTTTTCATCACTGAGACATGGAATGAAGTGGGGAT 528
QY 155 PheGlyLeuAlaThrGlnLeuLysMetProHisGlnLysHisTyrThrLeuCysGlyThr 174
529 TTTGGCTGGCAGCCCGGTGGAGCTCGGAGCAGAGAGGAAGAACACCATCTGTGGCACC 588
QY 175 ProAsnTyrIleSerProGluIleAlaThrArgSerAlaHisGlyLeuGluSerAspVal 194
589 CCCAACTATGTGGCTCCAGAAAGTGTCTGAGACAGGGCCACGGGCCCTGAACGGATGTA 648
QY 195 TTPSerLeuGlyCysMetPheTyrThrLeuLeuIleGlyArgProPheAspThrAsp 214
649 TGGTCACTGGGCTGTGTATGTACACGCTGCTCTCGGGAGGCCCTCTTGTAGACGGGT 708
QY 215 ThrValLysAsnThrLeuAsnLysValValLeuAlaAspTyrGluMetProSerPheLeu 234
709 GACCTGAAGGAGACGTACCGCTGCATCAAGCAGGTTCACTACACGCTGCTGCCACGCTC 768
QY 235 SerIleGluAlaLysAspLeuIleHisGlnLeuLeuArgAsnProAlaAspArgLeu 254
769 TCACTGCTCCCGCAGCTCTCTGGCGCCCTCTCTCGGGCTCACCCTGAGACGCGCCC 828
QY 255 SerLeuSerSerValLeuAspHisProPheMetSerArgAsnSerSerThrLysSerLys 274
829 TCTATTGACCATCTCGCCATGACTTCTTTACCAAG----- 867
QY 275 AspLeuGlyThrValGluAspSerIleAspSerGlyHisAlaThrIleSerThrAlaIle 294
868 -----GGCTACACCCCGATCGACTC-----CCTATCAGCAGCTGCGTG 906
QY 295 ThrAlaSerSerThr-----SerIleSerGly 304
907 ACAGTCCCGACACCTGACACCCCCCAACCCAGCTAGGAGTCTGTTGGCCAAAGTTACCAAG 966
QY 305 SerLeuPheAspLysArg 311
967 AGCCTCTTTGGCAGAAAGAG 987
Db 967 AGCCTCTTTGGCAGAAAGAG 987

RESULT 15
US-10-305-720-1147
; Sequence 1147, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressi
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1147
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g1488262
US-10-305-720-1147

Alignment Scores:
Pred. No.: 1e-45 Length: 2169
Score: 590.50 Matches: 115
Percent Similarity: 57.33% Conservative: 61
Best Local Similarity: 37.46% Mismatches: 106
Query Match: 11.63% Indels: 25

```
DB: 17 Gaps: 4
US-10-026-021-2 (1-970) x US-10-305-720-1147 (1-2169)
QY 15 GlyAsnLeuLeuGlyLysGlySerPheAlaGlyValTyrArgAlaGluSerIleHisThr 34
   |||||
Db 112 GCGCGCTTGTGGCAAGGGGGCTTCGCCGCTCTACGAGGCCACTGACACAGAGACT 171
QY 35 GlyLeuGluValAlaIleLysMetIleAspLysLysAlaMetTyrLysAlaGlyMetVal 54
   |||||
Db 172 GCGAGCGCTACGCTGTCAAGTCATCCCGCAGAGCCGCGCTGCCCAAGCCGATCAGCGC 231
QY 55 GlnArgValGlnAsnGluValLysIleHisCysGlnLeuLysHisProSerIleLeuGlu 74
   |||||
Db 232 GAGAGATCCCTAATGAGATTGAGCTGCACCGAGACCTGCAGCACCGCCACATCGTGGCT 291
QY 75 LeuTyrAsnTyrPheGluAspSerAsnTyrValTyrLeuValLeuGluMetCysHisAsn 94
   |||||
Db 292 TTTTCGCACCACTTTGAGAGCGCTGACAACTACTCATTTCTTGGAGCTCTGCAGCCGA 351
QY 95 GlyGluMetAsnArgTyrLeuLysAsnArgValLysProPheSerGluAsnGluAlaArg 114
   |||||
Db 352 AAGTCCCTGGCCCACTCTGGGAAGCCCGG---CACACCTGTTGGAGCCAGAGTGGCG 408
QY 115 HisPheMetHisGlnIleThrGlyMetLeuTyrLeuHisSerHisGlyIleLeuHis 134
   |||||
Db 409 TACTACCTGGCGCAGATCTTCTGGCTCAAGTACTTGCACCGCGCGGCATCTTGGCAC 468
QY 135 ArgAspLeuThrLeuSerAsnLeuLeuLeuThrArgAsnMetAsnIleLysIleAlaAsp 154
   |||||
Db 469 CGGACCTCAAGTTGGAAATTTTTCATCTACTGAGAACATGGAACCTGAAGTGGGGAT 528
QY 155 PheGlyLeuAlaThrGlnLeuLysMetProHisGluLysHisTyrThrLeuCysGlyThr 174
   |||||
Db 529 TTTGGCTGGCGCGCGGTGGAGCTCCGGAGCAGAGGAGAACACCATCTGTGGCAC 588
QY 175 ProAsnTyrIleSerProGluIleAlaThrArgSerAlaHisGlyLeuGluSerAspVal 194
   |||||
Db 589 CCCACTATGTGGCTCCAGAGTGTGCTGTGACAGAGGCCACCGCCCTGAAGCGGATGTA 648
QY 195 TrpSerLeuGlyCysMetPheTyrThrLeuLeuIleGlyArgProProPheAspThrAsp 214
   |||||
Db 649 TGGTCACTGGGCTGTGTATGATGACAGCTGCTCTCGGGAGGCCCTCCCTTTGAGAGCGCT 708
QY 215 ThrValLysAsnThrLeuAsnLysValValLeuAlaAspTyrGluMetProSerPheLeu 234
   |||||
Db 709 GACCTGAAGGAGAGCTACCGCTGCATCAAGCAGAGGTTCACTACGCTGCCCTGCCAGCCTC 768
QY 235 SerIleGluAlaLysAspLeuIleHisGlnLeuLeuArgArgAsnProAlaAspArgLeu 254
   |||||
Db 769 TCACCTGCCCTGCCGCGAGCTCTGCGCGCCATCTTCGGGCTCACCCCGAGAGCCGCC 828
QY 255 SerLeuSerSerValLeuAspHisProPheMetSerArgAsnSerSerThrLysSerLys 274
   |||||
Db 829 TCTATTGACCATCTCGGCATGACTTCTTTACCAAG----- 867
QY 275 AspLeuGlyThrValGluAspSerIleAspSerGlyHisAlaThrIleSerThrAlaIle 294
   |||||
Db 868 -----GGCTACACCCCGATCGACTC-----CCTATCAGCAGCTGCGTG 906
QY 295 ThrAlaSerSerSerThr-----SerIleSerGly 304
   |||||
Db 907 ACAGTCCAGACCTGACACCCCAACCCAGCTAGAGTCTGTGTGGCAAGATTACCAAG 966
QY 305 SerLeuPheAspLysArgArg 311
   |||||
Db 967 AGCCTCTTTGGCAGAGAAG 987
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Search completed: September 8, 2005, 00:16:08
Job time : 1517 secs